

RL Vaccine 11:438-444(1993).
 CC -!- FUNCTION: This protein directs fusion of viral and cellular
 CC membranes.
 CC -!- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2
 CC LINKED BY A DISULFIDE BOND.
 CC -!- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
 CC family.
 CC -----
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 CC -----
 CC EMBL: M21849; AAA42878.1; -
 CC EMBL: X65509; CA946481.1; -
 CC PIR: J50321; VGNZCD.
 CC PIR: S21382; S21382.
 CC HSSP: P04849; LSVP.
 CC InterPro: IPR000776; Fusion gly.
 CC Pfam: PF00523; fusion_gly; 1.
 CC Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal.
 CC SIGNAL 1 ?
 CC CHAIN 1 ?
 CC CHAIN 2 ?
 CC CHAIN 3 ?
 CC TRANSMEM 606 629
 CC DISULFID 180 307
 CC CARBOHYD 62 62
 CC CARBOHYD 141 141
 CC CARBOHYD 173 173
 CC CARBOHYD 179 179
 CC CONFLICT 3 3
 CC CONFLICT 140 140
 CC CONFLICT 152 152
 CC CONFLICT 171 171
 CC CONFLICT 174 174
 CC CONFLICT 662 662
 CC SEQUENCE 662 AA; 72970 MW; FB2C81C9797805F0 CRC64;
 Query Match 37.9%; Score 66; DB 1; Length 662;
 Best Local Similarity 73.7%; Pred. No. 0.14;
 Matches 14; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 15 SLKLLSEIKGVIVHLEGV 33
 Db 396 SYPTUSEVKGIVHLEAV 414
 RESULT 8
 ID -GON1 SPAAU STANDARD; PRT; 95 AA.
 AC P51979; Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Gonadoliberin I precursor (Gonadotropin-releasing hormone I) (GNRH-I)
 DE (LH-RH I) (Luliberin I) (SBNRH).
 GN GNRH1.
 OS Sparus aurata (Gilthead sea bream).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes; Percoidae;
 OC Sparidae; Sparus.
 OX NCBI_TaxID=8175;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=95268499; PubMed=7749463;
 RA Gethilf Y., Elizur A., Chow M., Chen T.T., Zohar Y.;
 RT "Molecular cloning and characterization of a novel gonadotropin-

RT releasing hormone from the gilthead seabream (Sparus aurata).";
 RL Mol. Mar. Biol. Biotechnol. 4:27-35(1995).
 RN [2]
 RP SEQUENCE OF 26-35.
 RC TISSUE=Brain;
 RX MEDLINE=95083645; PubMed=7991588;
 RA Powell J.F.F., Zohar Y., Elizur A., Park M., Fischer W.H.,
 RA Craig A.G., Rivier J.E., Lovejoy D.A., Sherwood N.M.;
 RT "Three forms of gonadotropin-releasing hormone characterized from
 RT brains of one species.";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:12081-12085(1994).
 CC -!- FUNCTION: Stimulates the secretion of gonadotropins.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- MASS SPECTROMETRY: MW=1113.6; METHOD=MAJDI; RANGE=26-35.
 CC -!- SIMILARITY: Belongs to the GNRH family.
 CC -----
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 CC -----
 CC EMBL: U30320; AAA75469.1; -
 CC InterPro: IPR002012; GNRH.
 CC InterPro: IPR004079; GonadoliberinI.
 CC Pfam: PF00446; GNRH; 1.
 CC PRINTS: PR01541; GONADOLIBRNI.
 CC PROSITE: PS00473; GNRH; 1.
 CC Cleavage on pair of basic residues; Hormone; Amidation; Hypothalamus;
 CC Signal; Multigene family; Pyrrolidone carboxylic acid.
 CC SIGNAL 1 95
 CC CHAIN 26 95
 CC CHAIN 26 95
 CC PEPTIDE 26 35
 CC PEPTIDE 39 95
 CC MOD RES 26 26
 CC MOD RES 35 35
 CC SEQUENCE 95 AA; 10753 MW; 49313FD6FD687DA CRC64;
 Query Match 37.6%; Score 65.5; DB 1; Length 95;
 Best Local Similarity 45.5%; Pred. No. 0.019;
 Matches 15; Conservative 3; Mismatches 14; Indels 1; Gaps 1;
 QY 2 HWSYGLRPGSSGSPSLKLLSEIKGVIVHLEGV 34
 Db 27 HWSYGLSPGKG-RDLDSLSDTLGNIIERPHVD 58
 RESULT 9
 ID -VGLF RINDK STANDARD; PRT; 546 AA.
 AC P12574;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
 DE Fusion glycoprotein F1].
 GN F.
 OS Rinderpest virus (strain Kabete O) (RDV).
 OS Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Paramyxoviridae; Paramyxovirinae; Morbillivirus.
 OX NCBI_TaxID=11242;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88322864; PubMed=3413983;
 RA Hsu D., Yamanaka M., Miller J., Dale B., Grubman M., Vilma T.;
 RT "Cloning of the fusion gene of rinderpest virus: comparative sequence
 RT analysis with other morbilliviruses.";
 RL Virology 166:149-153(1988).
 CC -!- FUNCTION: This protein directs fusion of viral and cellular
 CC membranes.
 CC -!- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2

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CC CC LINKED BY A DISULFIDE BOND.
CC CC -!- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
CC CC family.
CC CC -----
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CC CC or send an email to license@isb-sib.ch).
CC CC -----
CC CC EMBL; M21514; AAA47400.1; --
CC CC PIR; A31051; VGNZK.
CC CC HSSP; P04849; 1SVF.
CC CC InterPro; IPR000776; Fusion gly.
CC CC Pfam; PF00523; fusion_gly; 1.
CC CC KW Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal.
CC CC FT SIGNAL 1 19
CC CC FT CHAIN 20 546 FUSION GLYCOPROTEIN F0.
CC CC FT CHAIN 20 108 F2 PROTEIN.
CC CC FT CHAIN 109 546 F1 PROTEIN.
CC CC FT DOMAIN 104 108 ARG-RICH (BASIC).
CC CC FT TRANSMEM 109 133 POTENTIAL.
CC CC FT TRANSMEM 484 513 ARG/LYS-RICH (BASIC).
CC CC FT DOMAIN 514 517 LINKAGE BETWEEN F2 & F1 (POTENTIAL).
CC CC FT DISULFID 64 191 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CC FT CARBOHYD 25 25 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CC FT CARBOHYD 57 57 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CC FT CARBOHYD 63 63 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CC FT CARBOHYD 518 518 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CC SEQUENCE 546 AA; 58662 MW; 476D74DC1B8CFCF CRC64;
CC CC
CC CC Query Match 37.4%; Score 65; DB 1; Length 546;
CC CC Best Local Similarity 86.7%; Pred. No. 0.16;
CC CC Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
CC CC
QY 19 LSEIKGVIVHLEGV 33
DB 284 LSEIKGVIVHLEGV 298
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RESULT 10
VGLF PHODV
ID VGLF PHODV STANDARD; PRT; 631 AA.
AC F28886;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
DE Fusion glycoprotein F1].
GN F.
OS Phocine distemper virus (PDV).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX NCBI_TaxID=11240;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Isolate DK88-4A;
RX MEDLINE=92113538; PubMed=1765768;
RA Koevamees J., Blixenkron-Moeller M., Sharma B., Oervell C.,
RA Norby E.;
RT "The nucleotide sequence and deduced amino acid composition of the
RT haemagglutinin and fusion proteins of the morbillivirus phocid
RT distemper virus."
RL J. Gen. Virol. 72:2959-2966(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Ulster/88;
RX MEDLINE=92398437; PubMed=1524494;
RA Curran M.D., Lu Y.J., Rima B.K.;
RA "The fusion protein gene of phocine distemper virus: nucleotide and
RT deduced amino acid sequences and a comparison of morbillivirus fusion

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RT proteins.";
RL Arch. Virol. 126:159-169(1992).
RN [3]
RP SEQUENCE OF 95-631 FROM N.A.
RC STRAIN=Ulster/88;
RX MEDLINE=91089508; PubMed=2264246;
RA Curran M.D., Loan D.O., Rima B.K., Kennedy S.;
RA "Nucleotide sequence analysis of phocine distemper virus reveals its
RT distinctness from canine distemper virus."
RL Rec. Rec. 127:430-431(1990).
CC -!- FUNCTION: This protein directs fusion of viral and cellular
CC membranes.
CC -!- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2
CC LINKED BY A DISULFIDE BOND.
CC -!- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
CC family.
CC CC -----
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CC CC or send an email to license@isb-sib.ch).
CC CC -----
CC CC EMBL; D10371; BAA01206.1; --
CC CC PIR; A48346; A48346.
CC CC PIR; J01368; VGN2PD.
CC CC HSSP; P04849; 1SVF.
CC CC InterPro; IPR000776; Fusion gly.
CC CC Pfam; PF00523; fusion_gly; 1.
CC CC KW Glycoprotein; Fusion protein; Transmembrane; Envelope protein; Signal.
CC CC FT SIGNAL 1 631
CC CC FT CHAIN ? 631 FUSION GLYCOPROTEIN F0.
CC CC FT CHAIN ? 188 F2 PROTEIN.
CC CC FT CHAIN 194 631 F1 PROTEIN.
CC CC FT DISULFID 149 276 LINKAGE BETWEEN F2 & F1 (POTENTIAL).
CC CC FT TRANSMEM 89 106 POTENTIAL.
CC CC FT TRANSMEM 194 212 POTENTIAL.
CC CC FT TRANSMEM 575 595 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CC FT CARBOHYD 110 110 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CC FT CARBOHYD 142 142 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CC FT CARBOHYD 148 148 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CC FT CONFLICT 63 63 I -> V (IN REF. 2).
CC CC SEQUENCE 631 AA; 68873 MW; D1FC87CDD426E9B8 CRC64;
CC CC
CC CC Query Match 37.4%; Score 65; DB 1; Length 631;
CC CC Best Local Similarity 68.4%; Pred. No. 0.19;
CC CC Matches 13; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
CC CC
QY 15 SLKLSEIKGVIVHLEGV 33
DB 365 SYPTLSEVKGVVVHLEAV 383
-----
RESULT 11
GON1 MACMU
ID GON1 MACMU STANDARD; PRT; 67 AA.
AC P55247;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Progadoliberin I precursor [Contains: Gonadoliberin I (LH-RH I)
DE (Luteinizing hormone-releasing hormone I) (Gonadotropin-releasing
DE hormone I) (GnRH I) (Luliberin I); GnRH-associated peptide I]
DE (Fragment).
GN GNRH1 OR GNRH OR LHRH.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544;
RN [1]

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RP SEQUENCE FROM N.A.
RC TISSUE-Hypothalamus;
RX MEDLINE=9524501; PubMed=7545971;
RA Ma Y.J., Costa M.E., Ojeda S.R.;
RT "Developmental expression of the genes encoding transforming growth
RT factor alpha and its receptor in the hypothalamus of female rhesus
RT macaques."
RL Neuroendocrinology 60:346-359(1994).
CC -!- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates
CC the secretion of both luteinizing and follicle-stimulating
CC hormones.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the GnRH family.
CC
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CC
CC EMBL; S75918; AAB33096.1; -
CC PIR; 178541; 178541; -
CC InterPro; IPR002012; GnRH.
CC InterPro; IPR004079; GonadoliberinL.
CC Pfam; PF00446; GnRH; 1.
CC PRINTS; PR01541; GONADOLIBERNI.
CC PROSITE; PS00473; GnRH; 1.
CC Cleavage on pair of basic residues; Hormone; Amidation; Hypothalamus;
CC Signal; Pyrrolidone carboxylic acid.
CC NON_TER 1 1
CC SIGNAL <1 5 BY SIMILARITY.
CC CHAIN 6 >67 PROGONADOLIBERIN I.
CC PEPTIDE 6 15 GONADOLIBERIN I.
CC PEPTIDE 19 >67 GnRH-ASSOCIATED PEPTIDE I.
CC ACT_SITE 8 8 APPEARS TO BE ESSENTIAL FOR BIOLOGICAL
CC ACTIVITY (BY SIMILARITY).
CC MOD_RES 6 6 PYRROLIDONE CARBOXYLIC ACID (BY
CC SIMILARITY).
CC MOD_RES 15 15 AMIDATION (G-16 PROVIDE AMIDE GROUP) (BY
CC SIMILARITY).
CC NON_TER 67 67
CC SEQUENCE 67 AA; 7573 MW; 505394DAA261A3F2 CRC64;
Query Match 36.8%; Score 64; DB 1; Length 67;
Best Local Similarity 40.0%; Pred. No. 0.022;
Matches 10; Conservative 5; Mismatches 10; Indels 0; Gaps 0;
QY 2 HWSYGLRPGSGPSLKLSEIKGVI 26
Db 7 HWSYGLRPGGKRDANLMSDFQEV 31
RESULT 12
ID GON1_HUMAN STANDARD; PRT; 92 AA.
AC P01148;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DE Progonadoliberin I precursor (Contains: Gonadoliberin I (LH-RH I)
DE (luteinizing hormone-releasing hormone I) (Gonadotropin-releasing
DE hormone I) (GnRH I) (Luliberin I) (Gonadorelin); GnRH-associated
DE peptide I).
DE GN GNRH1 OR GNRH OR LHRH.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89366682; PubMed=2671939;

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RA Hayflick J.S., Adelman J.P., Seeburg P.H.;
RT "The complete nucleotide sequence of the human gonadotropin-releasing
RT hormone gene."
RL Nucleic Acids Res. 17:6403-6403 (1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=86094338; PubMed=2867548;
RA Adelman J.P., Mason A.J., Hayflick J.S., Seeburg P.H.;
RT "Isolation of the gene and hypothalamic cDNA for the common precursor
RT of gonadotropin-releasing hormone and prolactin release-inhibiting
RT factor in human and rat."
RL Proc. Natl. Acad. Sci. U.S.A. 93:179-183 (1986).
RN [3]
RP SEQUENCE FROM N.A., AND VARIANT SER-16.
RX MEDLINE=85012739; PubMed=6090951;
RA Seeburg P.H., Adelman J.P.;
RT "Characterization of cDNA for precursor of human luteinizing hormone
RT releasing hormone."
RL Nature 311:666-668 (1984).
RN [4]
RP SEQUENCE OF 24-33.
RX MEDLINE=83126573; PubMed=6760865;
RA Tan L., Rousseau P.;
RT "The chemical identity of the immunoreactive LHRH-like peptide
RT biosynthesized in the human placenta."
RL Biochem. Biophys. Res. Commun. 109:1061-1071 (1982).
RN [5]
RP VARIANT SER-16.
RX MEDLINE=99318093; PubMed=10391209;
RA Cargill M., Altschuler D., Ireland J., Sklar P., Ardlie K., Patil N.,
RA Shaw N., Lane C.R., Lim E.P., Kalyanaram N., Nemesh J., Ziaugra L.,
RA Friedland L., Rolfe A., Warrington J., Lipschutz R., Daley G.Q.,
RA Lander E.S.;
RT "Characterization of single-nucleotide polymorphisms in coding regions
RT of human genes."
RL Nat. Genet. 22:231-238 (1999).
RN [6]
RP ERRATUM.
RA Cargill M., Altschuler D., Ireland J., Sklar P., Ardlie K., Patil N.,
RA Shaw N., Lane C.R., Lim E.P., Kalyanaram N., Nemesh J., Ziaugra L.,
RA Friedland L., Rolfe A., Warrington J., Lipschutz R., Daley G.Q.,
RA Lander E.S.;
CC -!- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates
CC the secretion of both luteinizing and follicle-stimulating
CC hormones.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PHARMACEUTICAL: Available under the names Factrel (Ayerst Labs),
CC Lutrepulse or Lutrelle (Ferring Pharmaceuticals) and Relisorm
CC (Serono).
CC -!- SIMILARITY: Belongs to the GnRH family.
CC
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CC
CC EMBL; X01059; CAA25526.1; -
CC EMBL; M12578; AAA35916.1; -
CC EMBL; X15215; CAA33285.1; -
CC PIR; S05308; RHUG.
CC Genew; HGNC:4419; GNRH1.
CC MIM; 152760; -
CC GO; GO:0005625; C:soluble fraction; TAS.
CC GO; GO:0005883; F:luteinizing hormone-releasing factor activity; TAS.
CC GO; GO:0007267; P:cell-cell signaling; TAS.
CC GO; GO:0007275; P:development; TAS.
CC GO; GO:0008285; P:negative regulation of cell proliferation; TAS.
CC GO; GO:0007165; P:signal transduction; TAS.
CC InterPro; IPR002012; GnRH.

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InterPro: IPR004079; Gonadoliberin I.
PFam: PF00446; GNRH; 1.
PRINTS: PR01541; GONADOLIBERNI.
PROSITE: PS00473; GNRH; 1.
KW Cleavage on pair of basic residues; Hormone; Amidation; Hypothalamus;
Placenta; Pharmaceutical; Signal; Polymorphism;
Pyroglutamate carboxylic acid.
KW SIGNAL 1 23
FT CHAIN 24 92
FT CHAIN 24 92
FT PEPTIDE 24 33
FT PEPTIDE 37 92
FT ACT_SITE 26 26
FT MOD_RES 24 24
FT MOD_RES 33 33
FT MOD_RES 16 16
FT VARIANT 16 16
SQ SEQUENCE 92 AA; 10380 MW; 30A72221B076FA79 CRC64;
Query Match 36.8%; Score 64; DB 1; Length 92;
Best Local Similarity 40.0%; Pred. No. 0.031;
Matches 10; Conservative 5; Mismatches 10; Indels 0; Gaps 0;
QY 2 HWSYGLRPGSGPSLKILSEIKGVI 26
DB 25 HWSYGLRPGGKRDENLDSFQEIY 49
RESULT 13
VGLP_MEASI STANDARD; PRT; 529 AA.
ID VGLP_MEASI STANDARD; PRT; 529 AA.
AC F26031; Q83298;
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Fusion glycoprotein precursor [Contains: Fusion glycoprotein F2;
Fusion glycoprotein F1].
GN F.
OS Measles virus (strain IP-3-Ca) (Subacute sclerosing panencephalitis
virus).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Morbilliviruses.
OC NCBI_TaxID=11237;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92263801; PubMed=1585658;
RA Schmid A., Spielhofer P., Cattaneo R., Baczko K., Ter Meulen V.,
RT Billster M.A.,
RT "Subacute sclerosing panencephalitis is typically characterized by
alterations in the fusion protein cytoplasmic domain of the
persisting measles virus."
RL Virology 188:910-915(1992).
CC -1- FUNCTION: This protein directs fusion of viral and cellular
membranes.
CC -1- SUBUNIT: THE MATURE FORM IS A DIMER OF POLYPEPTIDES F-1 AND F-2
CC LINKED BY A DISULFIDE BOND.
CC -1- SIMILARITY: Belongs to the paramyxoviruses fusion glycoprotein
family.

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EMBL; X16566; CAA34567.1; -
DR EMBL; X16566; CAA34568.1; ALT_INIT.
DR HSSP; P04849; 1SVF.
DR InterPro: IPR000776; Fusion gly.
DR Pfam; PR00523; fusion gly; 1.
DR Glycovert: Fusion protein; Transmembrane; Envelope protein; Signal.

```

Query Match      35.6%; Score 62; DB 1; Length 89;
Best Local Similarity 25.4%; Pred. No. 0.058;
Matches 15; Conservative 7; Mismatches 9; Indels 28; Gaps 1

Qy 2 HWSYGLRPGSGSPSLK-----LSEIKGVIVHRLG 32
      |||||
Db 25 HWSYGLRPGGKQDTSLOMAYHETNEVALPELERLECVSPQSRINLVRGALMNWLEG 83
      : : : : :

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OM protein - protein search, using sw model

Run on: March 10, 2004, 08:58:54 ; Search time 12.7763 Seconds
(without alignments)
133.345 Million cell updates/sec

Title: US-09-848-834A-12
Perfect score: 169
Sequence: 1 DEKXIAKMEKASSVFNVNSGSLHWSYGLRPX 33

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/6C_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/6D_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	134.5	79.6	33	1	US-08-446-692-27
2	134.5	79.6	33	2	US-08-488-351A-27
3	89	52.7	21	1	US-08-186-266-6
4	89	52.7	21	1	US-08-446-692-48
5	89	52.7	21	2	US-08-488-351A-48
6	89	52.7	21	3	US-09-100-409A-54
7	89	52.7	21	4	US-08-464-496-17
8	89	52.7	21	4	US-08-788-822A-12
9	89	52.7	21	4	US-08-197-484-97
10	89	52.7	21	4	US-09-543-608A-39
11	89	52.7	21	5	PCT-US95-02121-97
12	89	52.7	21	5	PCT-US95-13841-20
13	86	50.9	423	2	US-08-760-797A-1
14	86	50.9	424	2	US-08-760-797A-3
15	86	50.9	424	3	US-08-932-929B-1
16	86	50.9	424	3	US-08-932-929B-3
17	82	48.5	412	1	US-08-313-288B-18
18	79	46.7	17	4	US-08-464-496-16
19	79	46.7	17	4	US-08-197-484-96
20	79	46.7	17	5	PCT-US95-02121-96
21	75	44.4	16	2	US-08-817-933A-7
22	73.5	43.5	20	1	US-08-465-167A-20
23	73.5	43.5	20	4	US-08-627-820-29
24	73.5	43.5	20	5	PCT-US92-07218-17
25	70	41.4	15	6	5169933-30
26	66	39.1	30	3	US-09-100-414B-71
27	66	39.1	30	3	US-09-303-323-71

Sequence 71, Appl
Sequence 73, Appl
Sequence 73, Appl
Sequence 73, Appl
Sequence 19, Appl
Sequence 19, Appl
Sequence 16, Appl
Sequence 12, Appl
Sequence 68, Appl
Sequence 68, Appl
Sequence 68, Appl
Sequence 4, Appl
Sequence 4, Appl
Sequence 4, Appl
Sequence 4, Appl
Sequence 10, Appl
Sequence 10, Appl

30 4 US-09-770-014-71
30 3 US-09-100-414B-73
30 3 US-09-303-323-73
30 4 US-09-770-014-73
16 1 US-08-465-167A-19
16 4 US-08-627-820-19
16 5 PCT-US92-07218-16
21 1 US-08-305-871A-12
30 3 US-09-100-414B-68
30 3 US-09-303-323-68
30 4 US-09-770-014-68
49 1 US-08-387-156-4
49 2 US-08-694-865-4
49 2 US-08-878-748-4
49 3 US-09-124-491-4
49 4 US-09-383-912-4
544 1 US-08-387-156-10
544 2 US-08-694-865-10

ALIGNMENTS

RESULT 1
US-08-446-692-27
; Sequence 27, Application US/08446692
; Patent No. 579551
; GENERAL INFORMATION:
; APPLICANT: Ladd, Anna
; APPLICANT: Wang, Chang Yi
; APPLICANT: Zamb, Timothy
; TITLE OF INVENTION: Immunogenic LHRH peptide constructs
; TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maria C.H. Lin
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,692
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria C.H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4146 US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)415-8745
; TELEFAX: (516)751-6849
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-446-692-27

Query Match 79.6%; Score 134.5; DB 1; Length 33;
Best Local Similarity 90.3%; Pred. No. 3e-13;
Matches 28; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
Qy 2 EKXIAKMEKASSVFNVNSGSLHWSYGLRP 32
Db 3 EKXIAKMEKASSVFNVNSGSLHWSYGLRP 32

```

RESULT 2
US-08-488-351A-27      Application US/08488351A
; Sequence 27, Patent No. 5843446
; GENERAL INFORMATION:
; APPLICANT: Ladd, Anna
; APPLICANT: Wang, Chang Yi
; APPLICANT: Zamb, Timothy
; TITLE OF INVENTION: Immunogenic LHRH peptide constructs
; TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maria C.H. Lin
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,351A
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/446,692
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/229,275
; FILING DATE: 14-APR-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/057,166
; FILING DATE: 27-APR-1992
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria C.H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4146 US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)415-8745
; TELEFAX: (516)751-6849
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-488-351A-27

Query Match      79.6%; Score 134.5; DB 2; Length 33;
Best Local Similarity 90.3%; Pred. No. 3e-13;
Matches 28; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY      2 EKKIAKMEKASSVFNVNNSGSLHWSYGLRP 32
DB      3 EKKIAKMEKASSVFNVNNSGGE-HWSYGLRP 32

RESULT 3
US-08-186-266-6
; Sequence 6, Application US/08186266
; Patent No. 5662907
; GENERAL INFORMATION:
; APPLICANT: KUBO, Ralph T.
; APPLICANT: GREY, Howard M.
; APPLICANT: SETTE, Alessandro
; APPLICANT: CELIS, Esteban

```

```

; TITLE OF INVENTION: INDUCTION OF ANTI-TUMOR CYTOTOXIC
; TITLE OF INVENTION: T LYMPHOCYTES IN HUMANS USING
; TITLE OF INVENTION: SYNTHETIC PEPTIDE EPITOPES
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/186,266
; FILING DATE: 25-JAN-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/159,339
; FILING DATE: 29-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 14137-50-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1-21
; OTHER INFORMATION: /note= "Plasmodium falciparum CS
; OTHER INFORMATION: protein at positions 378-398."
US-08-186-266-6

Query Match      52.7%; Score 89; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 EKKIAKMEKASSVFNVNNS 20
DB      3 EKKIAKMEKASSVFNVNNS 21

RESULT 4
US-08-446-692-48
; Sequence 48, Application US/08446692
; Patent No. 5759551
; GENERAL INFORMATION:
; APPLICANT: Ladd, Anna
; APPLICANT: Wang, Chang Yi
; APPLICANT: Zamb, Timothy
; TITLE OF INVENTION: Immunogenic LHRH peptide constructs
; TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:

```

ADDRESSEE: Maria C.H. Lin
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: US
ZIP: 10154-0053
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,692
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maria C.H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4146 US2
TELEPHONE: (212)415-8745
TELEFAX: (516)751-6849
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-446-692-48

Query Match 52.7%; Score 89; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EKXIAMEKASSVFVNVS 20
DB 3 EKXIAMEKASSVFVNVS 21

RESULT 5
US-08-488-351A-48
Sequence 48, Application US/08488351A
Patent No. 5843446
GENERAL INFORMATION:
APPLICANT: Ladd, Anna
APPLICANT: Wang, Chang Yi
APPLICANT: Zamb, Timothy
TITLE OF INVENTION: Immunogenic LHRH peptide constructs
TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Maria C.H. Lin
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: US
ZIP: 10154-0053
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,351A
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/446,692
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/229,275
FILING DATE: 14-APR-1994

CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/057,166
FILING DATE: 27-APR-1992
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maria C.H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4146 US2
TELEPHONE: (212)415-8745
TELEFAX: (516)751-6849
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-488-351A-48

Query Match 52.7%; Score 89; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EKXIAMEKASSVFVNVS 20
DB 3 EKXIAMEKASSVFVNVS 21

RESULT 6
US-09-100-409A-54
Sequence 54, Application US/09100409A
Patent No. 6090388
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: PEPTIDE COMPOSITION FOR
TITLE OF INVENTION: PREVENTION AND TREATMENT OF HIV INFECTION AND
TITLE OF INVENTION: IMMUNE DISORDERS
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
SOFTWARE: #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,409A
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME:
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 1151-4154
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-100-409A-54

Query Match 52.7%; Score 89; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;

RESULT 8
US-08-788-822A-12
; Sequence 12, Application US/08788822A
; Patent No. 6413935
; GENERAL INFORMATION:
; APPLICANT: Alexander, Jeffrey L.
; APPLICANT: Defrees, Shawn
; APPLICANT: Sette, Alessandro
; TITLE OF INVENTION: Induction of Immune Response Against
; TITLE OF INVENTION: Desired Determinants
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/788,822A
; FILING DATE: 23-JAN-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:

```

; APPLICATION NUMBER: US 60/010,510
; FILING DATE: 24-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 014137-009210US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-788-822A-12

Query Match 52.7%; Score 89; DB 4; Length 21;
Best Local Similarity 100.0%; Pred.No.1.le-06;
Matches 19; Conservative 0; Mismatches 0; Indels

QY 2 EKKIARQKQKASSVFNVVNS 20
   |||||
Db 3 EKKIARQKQKASSVFNVVNS 21
   |||||

RESULT 9
US-08-197-484-97
; Sequence 97, Application US/08197484
; Patent No. 6419931
; GENERAL INFORMATION:
; APPLICANT: VITIELLO, Maria A.
; APPLICANT: CHESTNUT, Robert W.
; APPLICANT: SETTE, Alessandro D.
; APPLICANT: CELIS, Esteban
; APPLICANT: GRAY, Howard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; TITLE OF INVENTION: CTL IMMUNITY
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/197,484
; FILING DATE: 16-FEB-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/935,811
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-26-4
; TELECOMMUNICATION INFORMATION:

```

TELEPHONE: (206) 467-9600
TELEFAX: (206) 623-6793
INFORMATION FOR SEQ ID NO: 97:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..21
OTHER INFORMATION: /note="Malaria circumsporozoite
US-08-197-484-97

Query Match 52.7%; Score 89; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EKXIAKMEKASSVFNVNS 20
DB 3 EKXIAKMEKASSVFNVNS 21

RESULT 10
US-09-543-608A-39
Sequence 39, Application US/09543608A
Patent No. 6602510

GENERAL INFORMATION:
APPLICANT: Fikes, John D.
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Celis, Esteban
APPLICANT: Keogh, Elissa A.
APPLICANT: Chesnut, Robert
APPLICANT: Epimmune Inc.
TITLE OF INVENTION: HLA Class I A2 Tumor Associated Antigen
TITLE OF INVENTION: Peptides and Vaccine Compositions
FILE REFERENCE: 018623-015710US
CURRENT APPLICATION NUMBER: US/09/543,608A
CURRENT FILING DATE: 2002-04-05
NUMBER OF SEQ ID NOS: 52
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 39
LENGTH: 21
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Plasmodium falciparum CS protein positions 378-398

Query Match 52.7%; Score 89; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EKXIAKMEKASSVFNVNS 20
DB 3 EKXIAKMEKASSVFNVNS 21

RESULT 11
PCT-US95-02121-97
Sequence 97, Application PC/TUS9502121
GENERAL INFORMATION:
APPLICANT:

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
TITLE OF INVENTION: CTL IMMUNITY
NUMBER OF SEQUENCES: 153
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02121
FILING DATE: 16-FEB-1995
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/197,484
FILING DATE: 16-FEB-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/935,811
FILING DATE: 26-AUG-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/874,491
FILING DATE: 27-APR-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,682
FILING DATE: 29-JAN-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/749,568
FILING DATE: 26-AUG-1991

ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14137-26-4PC

TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 467-9600
TELEFAX: (415) 543-5043

INFORMATION FOR SEQ ID NO: 97:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid

STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
FEATURE:

NAME/KEY: Peptide
LOCATION: 1..21
OTHER INFORMATION: /note="Malaria circumsporozoite
OTHER INFORMATION: 378-398"

PCT-US95-02121-97

Query Match 52.7%; Score 89; DB 5; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EKXIAKMEKASSVFNVNS 20
DB 3 EKXIAKMEKASSVFNVNS 21

RESULT 12

PCT-US95-13841-20
Sequence 20, Application PC/TUS9513841

GENERAL INFORMATION:
APPLICANT: United Biomedical Inc; Walfield, Alan M.;
APPLICANT: Wang, Chang Yi

TITLE OF INVENTION: Synthetic IGE Membrane Anchor
TITLE OF INVENTION: Peptide Immunogens for the Treatment of Allergy
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:

ADDRESSEE: Maria C.H. Lin
STREET: 345 Park Avenue
CITY: New York
STATE: NY

COUNTRY: USA
ZIP: 10154

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:

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/ APPLICATION NUMBER: PCT/US95/13841
/ FILING DATE: 25-OCT-1995
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/328,519
/ FILING DATE: 25-OCT-1994
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Lid, Maria C.H.
/ REGISTRATION NUMBER: 29,323
/ REFERENCE/DOCKET NUMBER: 1151-4117
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 212-758-4800
/ TELEFAX: 212-751-6849
/ TELEX: 421792
/ INFORMATION FOR SEQ ID NO: 20:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 21 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ PCT-US95-13841-20

Query Match 52.7%; Score 89; DB 5; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EKKIAMEKASSVFNVNVS 20
Db 3 EKKIAMEKASSVFNVNVS 21

RESULT 13
US-08-760-797A-1
; Sequence 1, Application US/08760797A
; Patent No. 5928902
; GENERAL INFORMATION:
; APPLICANT: De Wilde, Michel
; TITLE OF INVENTION: Hybrid Protein Between CS
; TITLE OF INVENTION: from Plasmodium and HBSAG
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Smithkline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/760,797A
; FILING DATE: 04-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/442,612
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Baumeister, Kirk
; REGISTRATION NUMBER: 33,833
; REFERENCE/DOCKET NUMBER: B45015-1C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5096
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 424 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-760-797A-3

Query Match 50.9%; Score 86; DB 2; Length 424;
Best Local Similarity 67.7%; Pred. No. 9.4e-05;
Matches 21; Conservative 0; Mismatches 4; Indels 6; Gaps 1;

QY 2 EKKIAMEKASSVFNVNVS 32
Db 171 EKKIAMEKASSVFNVNVS 195

RESULT 15
US-08-932-929B-1
; Sequence 1, Application US/08932929B
; Patent No. 6169171
; GENERAL INFORMATION:
; APPLICANT: De Wilde, Michel
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/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-760-797A-1

Query Match 50.9%; Score 86; DB 2; Length 423;
Best Local Similarity 85.7%; Pred. No. 9.3e-05;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 EKKIAMEKASSVFNVNVS 22
Db 174 EKKIAMEKASSVFNVNVS 194

RESULT 14
US-08-760-797A-3
; Sequence 3, Application US/08760797A
; Patent No. 5928902
; GENERAL INFORMATION:
; APPLICANT: De Wilde, Michel
; TITLE OF INVENTION: Hybrid Protein Between CS
; TITLE OF INVENTION: from Plasmodium and HBSAG
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Smithkline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/760,797A
; FILING DATE: 04-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/442,612
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Baumeister, Kirk
; REGISTRATION NUMBER: 33,833
; REFERENCE/DOCKET NUMBER: B45015-1C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5096
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 424 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-760-797A-3

Query Match 50.9%; Score 86; DB 2; Length 424;
Best Local Similarity 67.7%; Pred. No. 9.4e-05;
Matches 21; Conservative 0; Mismatches 4; Indels 6; Gaps 1;

QY 2 EKKIAMEKASSVFNVNVS 32
Db 171 EKKIAMEKASSVFNVNVS 195

RESULT 15
US-08-932-929B-1
; Sequence 1, Application US/08932929B
; Patent No. 6169171
; GENERAL INFORMATION:
; APPLICANT: De Wilde, Michel
```

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APPLICANT: Cohen, Joseph
TITLE OF INVENTION: Hybrid Protein Between CS
TITLE OF INVENTION: from Plasmodium and HBSAG
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/932,929B
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/760,797
FILING DATE: 04-DEC-1996
APPLICATION NUMBER: 08/442,612
FILING DATE: 17-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: B45015-1FWC2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 424 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-932-929B-1

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Query Match          50.9%; Score 86; DB 3; Length 424;
Best Local Similarity 85.7%; Pred. No. 9.4e-05;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY      2 EKKIAPMEKASVFNVNSGP 22
Db      175 EKKICKMERKCSVFNVNSRP 195

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Job time : 12.7763 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 10, 2004, 09:16:59 ; Search time 25.9377 Seconds
(without alignments)
268.645 Million cell updates/sec

Title: US-09-848-834A-12
Perfect score: 169
Sequence: 1 DEKIAKKEKASSFNVNNGSLHWSGLRPX 33

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 809742 seqs, 211153259 residues

Total number of hits satisfying chosen parameters: 809742

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA.*
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9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09D_PUBCOMB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query %	ID	Description
1	168	99.4	33	9	US-09-848-834A-12
2	157	92.9	51	9	US-09-848-834A-20
3	95	56.2	20	9	US-09-848-834A-3
4	95	56.2	36	9	US-09-848-834A-16
5	92.5	54.7	31	15	US-10-411-544-39
6	89	52.7	19	14	US-10-239-313A-54
7	89	52.7	21	10	US-09-932-165-1482
8	89	52.7	21	10	US-09-935-384-710
9	89	52.7	21	10	US-09-942-052-711
10	89	52.7	21	14	US-10-001-469-1404
11	89	52.7	21	14	US-10-128-711-97
12	89	52.7	21	14	US-10-116-118-33
13	89	52.7	21	14	US-10-062-109A-761
14	89	52.7	21	14	US-10-005-480A-761
15	89	52.7	21	14	US-10-277-292-652

Sequence 26, Appl
Sequence 652, Appl
Sequence 20, Appl
Sequence 2583, Appl
Sequence 25, Appl
Sequence 2, Appl
Sequence 52, Appl
Sequence 44, Appl
Sequence 4224, Appl
Sequence 39, Appl
Sequence 19, Appl
Sequence 23, Appl
Sequence 15, Appl
Sequence 17, Appl
Sequence 31, Appl
Sequence 11, Appl
Sequence 96, Appl
Sequence 53, Appl
Sequence 3, Appl
Sequence 38, Appl
Sequence 39, Appl
Sequence 41, Appl
Sequence 60, Appl
Sequence 64, Appl
Sequence 67, Appl
Sequence 59, Appl
Sequence 65, Appl
Sequence 66, Appl

ALIGNMENTS

RESULT 1
US-09-848-834A-12
; Sequence 12, Application US/09848834A
; Patent No. US20020076416A1
; GENERAL INFORMATION:
; APPLICANT: Apton Corporation
; TITLE OF INVENTION: Chimeric Peptide Immunogens
; FILE REFERENCE: 1102865-0047
; CURRENT APPLICATION NUMBER: US/09/848,834A
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: 60/202,328
; PRIOR FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 12
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeric peptide consisting of amino acid sequence 378-398 of t
; OTHER INFORMATION: Plasmodium falciparum CSP protein linked by a spacer to amino a
; OTHER INFORMATION: id sequence 2-10 of the GnRH hormone
; NAME/KEY: MOD RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: Amidated aspartic acid
; NAME/KEY: MOD RES
; LOCATION: (33)..(33)
; OTHER INFORMATION: Amidated glycine or glycineamide
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(20)
; OTHER INFORMATION: Amino acid sequence 378-398 of the Malaria
; OTHER INFORMATION: (Plasmodium falciparum) circumsporozoite
; OTHER INFORMATION: (CSP) protein
; NAME/KEY: PEPTIDE
; LOCATION: (21)..(24)
; OTHER INFORMATION: Spacer peptide
; NAME/KEY: PEPTIDE
; LOCATION: (25)..(33)

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; OTHER INFORMATION: Amino acid sequence 2-10 of the human GnRH hormone
US-09-848-834A-12

Query Match          99.4%; Score 168; DB 9; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.3e-17;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEKKIARMEKASSVFNVNNSGPSLHWSYGLRP 32
    |||||
Db 1 DEKKIARMEKASSVFNVNNSGPSLHWSYGLRP 32

RESULT 2
US-09-848-834A-20
; Sequence 20, Application US/09848834A
; Patent No. US20020076416A1
; GENERAL INFORMATION:
; APPLICANT: Aphton Corporation
; TITLE OF INVENTION: Chimeric Peptide Immunogens
; FILE REFERENCE: 1102865-0047
; CURRENT APPLICATION NUMBER: US/09/848,834A
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: 60/202,328
; PRIOR FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeric peptide consisting of amino acid sequence 1-10 of human
; OTHER INFORMATION: GnRH linked by a spacer to amino acid sequence 378-398 of Plasmod
; OTHER INFORMATION: ium falciparum circumsporozoite (CSP) protein
; NAME/KEY: MOD_RES
; LOCATION: (1)..(51)
; OTHER INFORMATION: Pyroglutamic acid or 5-oxoproline
; NAME/KEY: MOD_RES
; LOCATION: (51)..(51)
; OTHER INFORMATION: Amidated glycine or glycineamide
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(10)
; OTHER INFORMATION: Amino acid sequence 1-10 of the human GnRH hormone
; NAME/KEY: PEPTIDE
; LOCATION: (11)..(16)
; OTHER INFORMATION: Spacer peptide
; NAME/KEY: PEPTIDE
; LOCATION: (17)..(36)
; OTHER INFORMATION: Amino acid sequence 378-398 of the Plasmodium falciparum
; OTHER INFORMATION: circumsporozoite (CSP) protein
; NAME/KEY: PEPTIDE
; LOCATION: (37)..(42)
; OTHER INFORMATION: Spacer peptide
; NAME/KEY: PEPTIDE
; LOCATION: (43)..(51)
; OTHER INFORMATION: Amino acid sequence 2-10 of the human GnRH hormone
US-09-848-834A-20

Query Match          92.9%; Score 157; DB 9; Length 51;
Best Local Similarity 94.1%; Pred. No. 8.7e-16;
Matches 32; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 DEKKIARMEKASSVFNVNNSGPSLHWSYGLRP 32
    |||||
Db 17 DEKKIARMEKASSVFNVNNSGSPSLHWSYGLRP 50

RESULT 3
US-09-848-834A-3
; Sequence 3, Application US/09848834A
; Patent No. US20020076416A1
; GENERAL INFORMATION:
; APPLICANT: Aphton Corporation

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RESULT 5
US-10-411-544-39
; Sequence 39, Application US/10411544
; Publication No. US20030232758A1
; GENERAL INFORMATION:
; APPLICANT: St. George-Hyslop, Peter
; APPLICANT: McLaurin, JoAnne
; TITLE OF INVENTION: Immunological Methods and Compositions for the Treatment of Alzheimer's Disease
; FILE REFERENCE: LI01547
; CURRENT APPLICATION NUMBER: US/10/411,544
; CURRENT FILING DATE: 2003-04-10
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: chimeric sequence
US-10-411-544-39

Query Match      54.7%; Score 92.5; DB 15; Length 31;
Best Local Similarity 79.3%; Pred. No. 1.7e-06;
Matches 23; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 2 EKXIAKMEKASSVFNVNNSGSLHWS-YG 29
DB 3 EKXIAKMEKASSVFNVNNSGGRHDSGYG 31

RESULT 6
US-10-239-313A-54
; Sequence 54, Application US/10239313A
; Publication No. US20030175285A1
; GENERAL INFORMATION:
; APPLICANT: KLINGUER - HAMOUR, Christine
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: BECK, Alain
; APPLICANT: GOETSCH, Liliane
; TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM OF A PEPTIDE
; FILE REFERENCE: 343 727 - US
; CURRENT APPLICATION NUMBER: US/10/239,313A
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: FR 00/03711
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: PCT 01/70772
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 697
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Plasmodium malariae
US-10-239-313A-54

Query Match      52.7%; Score 89; DB 14; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EKXIAKMEKASSVFNVNNS 20
DB 1 EKXIAKMEKASSVFNVNNS 19

RESULT 7
US-09-932-165-1482
; Sequence 1482, Application US/09932165
; Publication No. US20030134784A1

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; GENERAL INFORMATION:
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: CHALLITA-EID, PIA M.
; APPLICANT: FARIS, MARY
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: APAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: HUBERT, RENE
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITZ, AVA
; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED "USEFUL IN THE TREATMENT AND DETECTION OF CANCER"
; FILE REFERENCE: 51158-20014.00
; CURRENT APPLICATION NUMBER: US/09/932,165
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/226,329
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 1508
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1482
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Plasmodium falciparum
US-09-932-165-1482

Query Match      52.7%; Score 89; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.5e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EKXIAKMEKASSVFNVNNS 20
DB 3 EKXIAKMEKASSVFNVNNS 21

RESULT 8
US-09-935-384-710
; Sequence 710, Application US/09935384
; Publication No. US2003016526A1
; GENERAL INFORMATION:
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: APAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: FARIS, MARY
; APPLICANT: GE, WANGMAO
; APPLICANT: JAKOBOVITZ, AVA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1H4 "USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND OTHER CANCERS"
; FILE REFERENCE: 51158-20033.00
; CURRENT APPLICATION NUMBER: US/09/935,384
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 783
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 710
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Plasmodium falciparum
US-09-935-384-710

Query Match      52.7%; Score 89; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.5e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EKXIAKMEKASSVFNVNNS 20
DB 3 EKXIAKMEKASSVFNVNNS 21

```

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RESULT 9
US-09-942-052-711
; Sequence 711, Application US/09942052
; Publication No. US20030170626A1
; GENERAL INFORMATION:
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
; TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20028-00
; CURRENT APPLICATION NUMBER: US/09/942,052
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 711
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Plasmodium falciparum
US-09-942-052-711

Query Match          52.7%; Score 89; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.5e-06; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 0;

QY 2 EKKIAMEKASSVFNVNS 20
DB 3 EKKIAMEKASSVFNVNS 21

RESULT 10
US-10-001-469-1404
; Sequence 1404, Application US/10001469
; Publication No. US20030091562A1
; GENERAL INFORMATION:
; APPLICANT: JAKOBOVITS, AVA
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: SAFFRAN, DOUGLAS
; APPLICANT: HUBERT, RENE
; APPLICANT: PARIS, MARY
; APPLICANT: CHALLITA-EID, PIA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED
; TITLE OF INVENTION: 101P2A11 USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20024-20
; CURRENT APPLICATION NUMBER: US/10/001,469
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: 60/157,902
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/291,118
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 09/680,728
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 2888
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1404
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Plasmodium falciparum
US-10-001-469-1404

Query Match          52.7%; Score 89; DB 14; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.5e-06; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 0;

QY 2 EKKIAMEKASSVFNVNS 20
DB 3 EKKIAMEKASSVFNVNS 21
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RESULT 11
US-10-128-711-97
; Sequence 97, Application US/10128711
; Publication No. US2003009634A1
; GENERAL INFORMATION:
; APPLICANT: VITIELLO, Maria A.
; APPLICANT: CHESTNUT, Robert W.
; APPLICANT: SETTE, Alessandro D.
; APPLICANT: CELIS, Esteban
; APPLICANT: GRAY, Howard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; TITLE OF INVENTION: CTL IMMUNITY
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/128,711
; FILING DATE: 22-Apr-2002
; CLASSIFICATION: Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/197,484
; FILING DATE: 16-FEB-1994
; APPLICATION NUMBER: US 07/935,811
; FILING DATE: 26-AUG-1992
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-26-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (206) 623-6793
; INFORMATION FOR SEQ ID NO: 97:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..21
; OTHER INFORMATION: /note= "Malaria circumsporozoite
; 378-398"
; SEQUENCE DESCRIPTION: SEQ ID NO: 97:
US-10-128-711-97

Query Match          52.7%; Score 89; DB 14; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.5e-06; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 0;

QY 2 EKKIAMEKASSVFNVNS 20
DB 3 EKKIAMEKASSVFNVNS 21
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RESULT 12
US-10-116-118-33
; Sequence 761, Application US/10116118
; Publication No. US20030143672A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Bid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Heteroclitic Analogs and Related Methods
; FILE REFERENCE: 2060.0090003
; CURRENT APPLICATION NUMBER: US/10/116,118
; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: US 60/166,529
; PRIOR FILING DATE: 1999-11-18
; PRIOR APPLICATION NUMBER: US 60/239,008
; PRIOR FILING DATE: 2000-10-06
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Plasmodium falciparum
US-10-116-118-33

Query Match          52.7%; Score 89; DB 14; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.5e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EKKIAKWEKASSVFNVNS 20
Db 3 EKKIAKWEKASSVFNVNS 21

RESULT 13
US-10-062-109A-761
; Sequence 761, Application US/10062109A
; Publication No. US20030165505A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Bid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; FILE REFERENCE: 51158-20062.01
; CURRENT APPLICATION NUMBER: US/10/062,109A
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 761
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-062-109A-761

Query Match          52.7%; Score 89; DB 14; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.5e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EKKIAKWEKASSVFNVNS 20
Db 3 EKKIAKWEKASSVFNVNS 21

RESULT 14
US-10-005-480A-761
; Sequence 761, Application US/10005480A
; Publication No. US20030191073A1
; GENERAL INFORMATION:
; APPLICANT: Agensys
; APPLICANT: Challita-Bid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; FILE REFERENCE: 51158-20062.00
; CURRENT APPLICATION NUMBER: US/10/005,480A
; CURRENT FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 761
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-005-480A-761

Query Match          52.7%; Score 89; DB 14; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.5e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EKKIAKWEKASSVFNVNS 20
Db 3 EKKIAKWEKASSVFNVNS 21

RESULT 15
US-10-277-292-652
; Sequence 652, Application US/10277292
; Publication No. US20030199470A1
; GENERAL INFORMATION:
; APPLICANT: FARIS, MARY
; APPLICANT: HUBERT, RENE
; APPLICANT: RAITANO, ARTHUR
; APPLICANT: AFAR, DANIEL
; APPLICANT: LEVIN, ELANA
; APPLICANT: CHALLITA-EID, PIA
; APPLICANT: JAKOBOWITZ, AYA
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
; FILE REFERENCE: 51158-20050.00
; CURRENT APPLICATION NUMBER: US/10/277,292
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US/09/935,430
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/227,098
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/282,739
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 700
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 652
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Plasmodium falciparum
US-10-277-292-652

Query Match          52.7%; Score 89; DB 14; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.5e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EKKIAKWEKASSVFNVNS 20
Db 3 EKKIAKWEKASSVFNVNS 21
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Wed Mar 10 10:34:15 2004

us-09-848-834a-12.open.rapb

Page 6

Search completed: March 10, 2004, 10:25:48
Job time : 25.9377 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 10, 2004, 08:58:48 ; Search time 49.6926 Seconds
(without alignments)
187.635 Million cell updates/sec

Title: US-09-848-834A-12
Perfect score: 169
Sequence: 1 DEKIAKMEKASSFNVNVSGLHWSYGLRPX 33

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	168	99.4	33	5 AAU11423	AAU11423 Synthetic
2	157	92.9	51	5 AAU11431	AAU11431 Synthetic
3	134.5	79.6	33	2 AAR62715	AAR62715 LHRH-cont
4	95	56.2	20	5 AAU11414	AAU11414 P. falcip
5	95	56.2	33	2 AAR83570	AAR83570 IGE CH4 r
6	95	56.2	36	5 AAU11427	AAU11427 Synthetic
7	89	52.7	19	4 AAR98951	AAR98951 Vaccine r
8	89	52.7	21	1 AAR91504	AAR91504 Sequence
9	89	52.7	21	2 AAR78920	AAR78920 Malaria c
10	89	52.7	21	2 AAR75955	AAR75955 P. falcip
11	89	52.7	21	2 AAR70912	AAR70912 Malaria c
12	89	52.7	21	2 AAR82586	AAR82586 Plasmodiu
13	89	52.7	21	2 AAR05612	AAR05612 Circumspo
14	89	52.7	21	2 AAR35440	AAR35440 T-cell st
15	89	52.7	21	2 AAY23252	AAY23252 Peptide d
16	89	52.7	21	3 AAV58777	AAV58777 Unidentif
17	89	52.7	21	3 AAV80071	AAV80071 Pathogen
18	89	52.7	21	3 AAV54553	AAV54553 T helper
19	89	52.7	21	4 AAR88457	AAR88457 Plasmodiu
20	89	52.7	21	4 AAR84447	AAR84447 Sequence
21	89	52.7	21	4 AAG84517	AAG84517 Plasmodiu
22	89	52.7	21	4 AAB99706	AAB99706 Plasmodiu
23	89	52.7	21	4 AAG88269	AAG88269 Plasmodiu
24	89	52.7	21	4 AAG62428	AAG62428 Plasmodiu
25	89	52.7	21	4 AAG89366	AAG89366 Plasmodiu

26	89	52.7	21	5 ABB94469	ABB94469 Plasmodiu
27	89	52.7	21	5 ABB78050	ABB78050 Loosely M
28	89	52.7	21	5 ABJ11372	ABJ11372 P falcipa
29	89	52.7	21	5 ABJ05781	ABJ05781 P falcipa
30	89	52.7	21	5 ABP51501	ABP51501 Malaria c
31	89	52.7	21	5 AAU95369	AAU95369 Plasmodiu
32	89	52.7	21	5 ABG34858	ABG34858 P. falcip
33	89	52.7	21	5 ABJ01952	ABJ01952 158FID7 r
34	89	52.7	21	5 AAU91545	AAU91545 P. falcip
35	89	52.7	21	5 ABJ16181	ABJ16181 Zinc tran
36	89	52.7	21	5 ABU72602	ABU72602 Plasmodiu
37	89	52.7	21	6 ABJ39281	ABJ39281 Plasmodiu
38	89	52.7	21	6 ABU98401	ABU98401 Plasmodiu
39	89	52.7	21	6 ABR01863	ABR01863 Circumspo
40	89	52.7	21	6 ABJ56921	ABJ56921 Plasmodiu
41	89	52.7	21	7 ADC71173	ADC71173 P falcipa
42	89	52.7	21	7 ADD84523	ADD84523 Plasmodiu
43	89	52.7	21	7 AD865914	AD865914 Human 161
44	89	52.7	21	7 AD966934	AD966934 P falcipa
45	89	52.7	22	2 AAR82077	AAR82077 Malaria C

ALIGNMENTS

RESULT 1
AAU11423
ID AAU11423 standard; peptide; 33 AA.

XX AAU11423;

DT 12-MAR-2002 (first entry)

XX Synthetic immunogen peptide 4.

XX Gonadotropin releasing hormone; GnRH; synthetic immunogen;
luteinising hormone releasing hormone; LHRH; contraceptive;
promiscuous helper T-cell peptide epitope; immunomic peptide epitope;
breast cancer; uterine cancer; gynaecological cancer; endometriosis;
uterine fibroid; benign prostatic hypertrophy; prostate cancer.

OS Plasmodium falciparum.

OS Mammalia.

OS Synthetic.

OS Chimeric.

XX Key Location/Qualifiers

FT Peptide 1..20

FT Peptide /note= "Malaria CSP protein (378-398 aa)"

FT Peptide 21..24

FT Peptide /note= "Spacer peptide"

FT Peptide 25..33

FT Modified-site 33 /note= "Gonadotropin releasing hormone epitope"

XX /note= "Amidated glycine or glycinamide"

WO200185763-A2.

15-NOV-2001.

04-MAY-2001; 2001WO-US014363.

05-MAY-2000; 2000US-0202328P.

(APHT-) APHTON CORP.

Grimes S, Michaeli D, Stevens VC;

WPI; 2002-049440/06.

Novel synthetic immunogen for inducing immune response against
gonadotropin releasing hormone, comprises fusion peptide having
promiscuous helper T-cell peptide epitope and immunomic peptide epitope

```

XX 05-MAY-2000; 2000US-0202328P.
XX (APHT-) APHTON CORP.
XX Grimes S, Michaeli D, Stevens VC;
XX WPI; 2002-049440/06.
XX
XX Novel synthetic immunogen for inducing immune response against
XX gonadotropin releasing hormone, comprises fusion peptide having
XX promiscuous helper T-cell peptide epitope and immunomimic peptide epitope
XX or its analog.
XX
XX Claim 11; Page 12-13; 43pp; English.
XX
XX The invention relates to a synthetic immunogen for inducing specific
XX antibodies against gonadotropin releasing hormone (GnRH also known as
XX luteinising hormone releasing hormone, LHRH) comprising a fusion peptide
XX which comprises a promiscuous helper T-cell peptide epitope and
XX immunomimic peptide epitope or its analogue. The synthetic immunogen is
XX useful inducing an immune response against GnRH in an animal subject, and
XX as such is useful as a contraceptive and in the treatment of diseases
XX such as cancer (of the breast, uterus and other gynaecological cancer),
XX endometriosis, uterine fibroids, benign prostatic hypertrophy and
XX prostate cancer. The immunogen is effective in eliciting high and
XX specific anti-GnRH antibody titres. The present sequence is a synthetic
XX immunogen of the invention
XX
XX SQ Sequence 51 AA;
XX
XX Query Match 92.9%; Score 157; DB 5; Length 51;
XX Best Local Similarity 94.1%; Pred. No. 2.3e-16;
XX Matches 32; Conservative 0; Mismatches 0; Indels 2; Gaps 1
XX
XX QY 1 DEKTKAEKASSVFNVN--SGPSLHWSYGLRP 32
XX |||||
XX DB 17 DEKTKAEKASSVFNVNSSGSPSLHWSYGLRP 50
XX |||||
XX
XX RESULT 3
XX ID AAR62715
XX AC AAR62715 standard; peptide; 33 AA.
XX AC AAR62715;
XX AC AC
XX DT 25-MAR-2003 (revised)
XX DT 10-SEP-1995 (first entry)
XX DE LHRH-containing immunogenic peptide.
XX
XX Helper T cell epitope; universal immune stimulator; invasin; haptin;
XX vaccine; LHRH; luteinising hormone releasing hormone; prostate;
XX androgen-dependent carcinoma; antitumour; infertility;
XX Plasmodium falciparum circumsporozoite.
XX
XX OS Synthetic.
XX
XX Key Location/Qualifiers
XX Domain 1..21
XX FT /note= "Plasmodium falciparum circumsporozoite helper T
XX cell epitope"
XX Domain 24..33
XX FT /note= "LHRH haptin"
XX
XX WO9425060-A1.
XX
XX 10-NOV-1994.
XX
XX 28-APR-1994; 94MO-US004832.
XX
XX 27-APR-1993; 93US-00057166.
XX 14-APR-1994; 94US-00292775.

```

XX (LADD//) LADD A E.
PA (WANG//) WANG C Y.
PA (ZAMB//) ZAMB T.
XX
XX Ladd AE, Wang CY, Zamb T;
XX WPI; 1994-357910/44.
XX Immunogenic luteinizing hormone releasing hormone peptide(s) - that
PT suppress LHRH activity in males and females.
PS Claim 8; Page 86; 213pp; English.
XX Synthetic immunogenic peptides are provided in which a universal immune
CC stimulator is linked to a peptide or protein hapten containing B cell
CC and/or cytotoxic T lymphocyte epitopes, giving a product which causes
CC potent immune responses to the coupled peptide or protein. The stimulator
CC consists of (A) a promiscuous helper T cell epitope (Th) which elicits an
CC immune response to the coupled peptide in members of a heterogeneous
CC population expressing diverse HLA phenotypes, and (B) an adjuvant peptide
CC sequence from the invasive protein of Yersinia. Spacer amino acid
CC sequences (e.g. Gly-Gly) can be provided between the invasin and Th
CC domains and between the immune stimulator and hapten components. When the
CC hapten is LHRH, then optionally the invasin domain can be omitted from
CC the immune stimulator component. The present sequence represents an LHRH-
CC containing, invasin-free immunogenic peptide as above which can be used
CC as a potent vaccine for treating e.g. prostatic hyperplasia, androgen-
CC dependent carcinoma, prostatic carcinoma, testicular carcinoma,
CC endometriosis, benign uterine tumours, recurrent functional ovarian
CC cysts, (severe) premenstrual syndrome or oestrogen-dependent breast
CC cancer, or for induction of infertility. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX Sequence 33 AA;
SQ

Query Match 79.6%; Score 134.5; DB 2; Length 33;
Best Local Similarity 90.3%; Pred. No. 3.8e-13;
Matches 28; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
XX
XX 2 EKXIAKMEKASSVFNVNSGSLHWSYGLRP 32
DB |||||
XX 3 EKXIAKMEKASSVFNVNSGGE-HWSYGLRP 32
DB |||||
XX
XX RESULT 4
XX AAU11414
XX ID AAU11414 standard; peptide; 20 AA.
XX AC AAU11414;
XX DT 12-MAR-2002 (first entry)
XX DE P. falciparum circumsporozoite protein, CSP, peptide.
XX KW Gonadotropin releasing hormone; GnRH; synthetic immunogen;
XX KW luteinizing hormone releasing hormone; LHRH; contraceptive;
XX KW promiscuous helper T-cell peptide epitope; immunomimic peptide epitope;
XX KW breast cancer; uterine cancer; gynaecological cancer; endometriosis;
XX KW uterine fibroid; benign prostatic hypertrophy; prostate cancer;
XX KW circumsporozoite protein; CSP.
XX OS Plasmodium falciparum.
XX PN WO200185763-A2.
XX PD 15-NOV-2001.
XX PF 04-MAY-2001; 2001WO-US014363.
XX PR 05-MAY-2000; 2000US-0202328P.
XX PS (APHT-) APHTON CORP.
XX

XX Grimes S, Michaeli D, Stevens VC;
PI WPI; 2002-049440/06.
XX
XX Novel synthetic immunogen for inducing immune response against
PT gonadotropin releasing hormone, comprises fusion peptide having
PT promiscuous helper T-cell peptide epitope and immunomimic peptide epitope
PT or its analog.
XX
XX Disclosure; Page 28; 43pp; English.
XX
XX The invention relates to a synthetic immunogen for inducing specific
CC antibodies against gonadotropin releasing hormone (GnRH) also known as
CC luteinizing hormone releasing hormone (LHRH) comprising a fusion peptide
CC which comprises a promiscuous helper T-cell peptide epitope and
CC immunomimic peptide epitope or its analogue. The synthetic immunogen is
CC useful inducing an immune response against GnRH in an animal subject, and
CC as such is useful as a contraceptive and in the treatment of diseases
CC such as cancer (of the breast, uterus and other gynaecological cancer),
CC endometriosis, uterine fibroids, benign prostatic hypertrophy and
CC prostate cancer. The immunogen is effective in eliciting high and
CC specific anti-GnRH antibody titres. The present sequence is a peptide
CC from circumsporozoite protein, CSP, a promiscuous helper T-cell peptide
CC epitope used in the immunogen of the invention
XX Sequence 20 AA;
SQ

Query Match 56.2%; Score 95; DB 5; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.3e-07;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 DEKKIAKMEKASSVFNVNS 20
DB |||||
XX 1 DEKKIAKMEKASSVFNVNS 20
DB |||||
XX
XX RESULT 5
XX AAR83570
XX ID AAR83570 standard; peptide; 33 AA.
XX AC AAR83570;
XX DT 13-JUN-1996 (first entry)
XX DE IGE CH4 region contg. peptide immunogen for treating allergies.
XX KW IGE; CH4; immunoglobulin; epsilon; immunogen; helper T cell; epitope;
XX KW vaccine; allergy; antibody; constant heavy chain.
XX OS Synthetic.
XX PN WO9526365-A1.
XX PD 05-OCT-1995.
XX PF 24-MAR-1995; 95WO-US003741.
XX PR 28-MAR-1994; 94US-00218461.
XX PR 25-OCT-1994; 94US-00328912.
XX PA (UNBI-) UNITED BIOMEDICAL INC.
XX PI Wang CY;
XX DR WPI; 1995-351297/45.
XX
XX Synthetic peptide-based immunogen contg. IGE CH4 peptide and helper T
PT cell epitope - useful for eliciting antibody prodn. for allergy
PT treatment.
XX
XX Claim 5; Page 72; 87pp; English.
XX

CC AAR82592-R82600 and AAR83560-R83581 are peptide immunogens that are
 CC useful in vaccines for treating allergic reactions. In the immunogens, an
 CC IgG CH4 peptide is attached C-terminally to a series of amino acids
 CC including a helper T cell epitope. The immunogen may also opt. contain a
 CC fatty acid or fatty acid derivative, an invasin domain or alpha-NH2. The
 CC immunogen produces high titres of antibodies to the effector site in
 CC human IgG heavy chain (the CH4 domain peptide) which inhibit mast cell
 CC activation and reduce allergen-induced IgE prodn. The immunogens may be
 CC used in either a radially branching multimeric form or a linearly
 CC arranged monomeric form
 XX
 SQ Sequence 33 AA;

Query Match 56.2%; Score 95; DB 2; Length 33;
 Best Local Similarity 100.0%; Pred. No. 4.3e-07; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0;

QY 2 EKXIARMEKASSVFNVNSG 21
 Db 3 EKXIARMEKASSVFNVNSG 22

RESULT 6
 AAU11427
 ID AAU11427 standard; peptide; 36 AA.

AC AAU11427;
 DT 12-MAR-2002 (first entry)
 DE Synthetic immunogen peptide 8.

CC Gonadotrophin releasing hormone; GnRH; synthetic immunogen;
 CC luteinising hormone releasing hormone; LHRH; contraceptive;
 CC promiscuous helper T-cell peptide epitope; immunomimic peptide epitope;
 CC breast cancer; uterine cancer; gynaecological cancer; endometriosis;
 CC uterine fibroid; benign prostatic hypertrophy; prostate cancer.

OS Plasmodium falciparum.
 OS Mammalia.
 OS Synthetic.
 OS Chimeric.

Key Location/Qualifiers
 FT Peptide 1..10
 FT Misc-difference 1 /note= "Gonadotrophin releasing hormone epitope"
 FT /label= OTHER
 FT Peptide 11..16 /note= "Pyro-glutamic acid or 5-oxo proline"
 FT Peptide 17..36 /note= "Spacer peptide"
 FT Peptide 17..36 /note= "Malaria CSP protein (378-398 aa)"

WO200185763-A2.
 15-NOV-2001.
 04-MAY-2001; 2001WO-US014363.
 05-MAY-2000; 2000US-0202328P.
 (APHT-) APHTON CORP.

Grimes S, Michaeli D, Stevens VC;
 WPI; 2002-049440/06.

Novel synthetic immunogen for inducing immune response against
 PT gonadotropin releasing hormone, comprises fusion peptide having
 PT promiscuous helper T-cell peptide epitope and immunomimic peptide epitope
 PT or its analog.

PS Claim 11; Page 10; 43pp; English.

CC The invention relates to a synthetic immunogen for inducing specific
 CC antibodies against gonadotropin releasing hormone (GnRH) also known as
 CC luteinising hormone releasing hormone, LHRH) comprising a fusion peptide
 CC which comprises a promiscuous helper T-cell peptide epitope and
 CC immunomimic peptide epitope or its analogue. The synthetic immunogen is
 CC useful inducing an immune response against GnRH in an animal subject, and
 CC as such is useful as a contraceptive and in the treatment of diseases
 CC such as cancer (of the breast, uterus and other gynaecological cancer),
 CC endometriosis, uterine fibroids, benign prostatic hypertrophy and
 CC prostate cancer. The immunogen is effective in eliciting high and
 CC specific anti-GnRH antibody titres. The present sequence is a synthetic
 CC immunogen of the invention

SQ Sequence 36 AA;

Query Match 56.2%; Score 95; DB 5; Length 36;
 Best Local Similarity 100.0%; Pred. No. 4.8e-07; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0;

QY 1 DEKKIARMEKASSVFNVNS 20
 Db 17 DEKKIARMEKASSVFNVNS 36

RESULT 7
 AAM98951
 ID AAM98951 standard; peptide; 19 AA.

AC AAM98951;

DT 07-DEC-2001 (first entry)

DE Vaccine related MHC ligand peptide SEQ ID NO:54.

CC Glutamic acid; glutamine; vaccine; major histocompatibility complex; MHC;
 CC immunomodulator; antiallergic; endocrine; neuroprotectant; virucidal;
 CC bactericidal; antiparasitic; fungicidal; cytostatic; medicine;
 CC pharmaceutical; immune disorder; immune deficiency; autoimmune;
 CC hypersensitivity; allergy; graft rejection; infection; hormonal disorder;
 CC central nervous system disease; cancer; melanoma; anti-melanoma vaccine;
 CC human immunodeficiency virus.

OS Plasmodium malariae.

PN WO200170772-A2.

PD 27-SEP-2001.

PF 22-MAR-2001; 2001WO-FR000872.

PR 23-MAR-2000; 2000FR-00003711.

PA (FABR) FABRE MEDICAMENT SA PIERRE.

PI Klinguer-Hamour C, Corvaia N, Beck A, Goetsch L;

WPI; 2001-611470/70.

PT Stabilized pharmaceutical containing N-terminal glutamic acid or
 PT glutamine, useful e.g. in anti-melanoma vaccines, is an addition salt
 PT with strong acid.

PS Claim 9; Page 39; 149pp; French.

CC The present invention describes a pharmaceutical compound (I) that
 CC contains an N-terminal glutamic acid (Glu) or glutamine (Gln) residue in
 CC the form of an addition salt with a strong, physiologically acceptable
 CC acid (II). Also described are: (a) a pharmaceutical composition
 CC containing at least one (I); (b) a vaccine containing at least one (I)
 CC where this is a major histocompatibility complex (MHC) ligand (Ia); (c) a
 CC method for in vitro diagnosis of diseases associated with the presence of

CC (Ia); (d) a kit for method (c) that includes a (Ia); and (e) a process
 CC for preparing (I). (I) has immunomodulator, endocrine, antiallergic,
 CC neuroprotectant, virucidal, bactericidal, antiparasitic, fungicidal, and
 CC cytostatic activities. (I) are useful, in human or veterinary medicine,
 CC in pharmaceutical compositions (for treating immune disorders, e.g.
 CC immune deficiency, autoimmune states, hypersensitivity, allergy, graft
 CC rejection, infection, hormonal disorders and central nervous system
 CC diseases), also, where (I) is a MHC ligand (Ia), in vaccines for
 CC treatment or prevention of: (i) viral, bacterial, parasitic or fungal
 CC infections; or (ii) of cancers. A particular application is in anti-
 CC melanoma vaccines. (I) are also useful for in vitro diagnosis of diseases
 CC associated with interactions between MHC and (I), e.g. melanoma and human
 CC immunodeficiency virus infection. AAM9898 to AAM9952 represent peptides
 CC which can be used in pharmaceutical compounds from the present invention
 XX
 XX SQ Sequence 19 AA;

Query Match 52.7%; Score 89; DB 4; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.8e-06;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EKXIAMEKASSVFNVNS 20
 Db 1 EKXIAMEKASSVFNVNS 19

RESULT 8
 AAP91504
 ID AAP91504 standard; peptide; 21 AA.

XX AAP91504;

XX 13-MAR-1992 (first entry)

XX Sequence of modified Plasmodium circumsporozoite T-cell epitope CS.T3.

XX Circumsporozoite peptide; T-cell epitope; immunogenic composition;
 XX vaccine.

XX Plasmodium falciparum.

XX Key Location/Qualifiers

FT Misc-difference 1..2 /note= "May be H-Asp-Ile, H-Ile, or H."

FT Misc-difference 19..21

FT "/note= "May be Val-Asn-Ser-OH, Val-Asn-OH, Val-OH or -OH

FT "

XX EP343460-A.

XX 29-NOV-1989.

XX 12-MAY-1989; 89EP-00108618.

XX 24-MAY-1988; 89GB-00012214.

XX (HOFF) HOFFMANN-LA ROCHE AG.

XX Sinigaglia F;

XX WPI; 1989-349561/48.

XX Modified Plasmodium CS peptide - used as a universally recognised T-cell
 FT epitope in vaccines to elicit an immune response against pathogenic
 FT agents.

XX Claim 1; Page 16; 23pp; English.

XX Peptide CS.T3 (residues 1-21) corresponds to residues 378-398 of the CS
 CC protein from P. falciparum but contains 2 Ala residues in place of the
 CC native protein's Cys residues at positions 384 and 389. Also claimed is
 CC AAP91504 (or modified forms, see FT) associated with an antigenic
 CC structure representing a B-cell epitope, pref. a multiple antigenic

CC peptide, esp. multimers of the repeat sequences NANP present in P.
 CC falciparum CS protein
 XX Sequence 21 AA;

Query Match 52.7%; Score 89; DB 1; Length 21;
 Best Local Similarity 100.0%; Pred. No. 2.1e-06;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EKXIAMEKASSVFNVNS 20
 Db 3 EKXIAMEKASSVFNVNS 21

RESULT 9

AAR78920
 ID AAR78920 standard; peptide; 21 AA.

XX AAR78920;

XX 27-AUG-2003 (revised)

DT 25-MAR-2003 (revised)

DT 27-MAR-1996 (first entry)

XX Malaria circumsporozoite 378-398 helper T lymphocyte epitope.

XX 378-398; cytotoxic T; CTL; epitope; helper T; HTL; cell; lymphocyte;
 KW antigens; treatment; disease prevention; tumours; viruses; parasites;
 KW malaria circumsporozoite; hepatitis B.

XX Plasmodium falciparum.

XX WO952317-A1.

XX 24-AUG-1995.

XX 16-FEB-1995; 95WO-US002121.

XX 16-FEB-1994; 94US-00197484.

XX (CYTE-) CYTEL CORP.

XX Vitello MA, Chesnut RW, Sette AD, Celis E, Grey H;

XX WPI; 1995-302545/39.

XX Compn. inducing cytotoxic T lymphocyte response to pref. viral,
 FT bacterial, parasitic or tumour antigens - useful in the treatment and
 FT prevention of diseases associated with the antigen e.g. hepatitis B.

XX Disclosure; Page 29; 109pp; English.

XX A compsn. which induces a cytotoxic T lymphocyte (CTL) response to an
 CC antigen (Ag) in a mammal comprises, a CTL Ag response inducing peptide
 CC and a lipid conjugated helper T cell inducing peptide (i.e. AAR78918-
 CC R78922). The compsn. induces a CTL response to bacterial, viral or tumour
 CC Ags, and is therefore useful in the treatment and prevention of diseases
 CC associated with the Ag, e.g. hepatitis B. (Updated on 25-MAR-2003 to
 CC correct PI field.) (Updated on 27-AUG-2003 to correct OS field.)
 XX

XX SQ Sequence 21 AA;

Query Match 52.7%; Score 89; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 2.1e-06;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EKXIAMEKASSVFNVNS 20
 Db 3 EKXIAMEKASSVFNVNS 21

RESULT 10
 AAR75955

ID AAR75955 standard; peptide; 21 AA.
 XX AC AAR75955;
 XX DT 06-MAR-1996 (first entry)
 XX PA P. falciparum CS protein epitope residues 378-398.
 XX DE
 XX KW MAGE-3; melanoma antigen; vaccine; immune response; immunogenic peptide;
 XX KW cytotoxic T lymphocyte response; CTL; melanoma; breast cancer; antibody.
 XX OS Plasmodium falciparum.
 XX PN WO9519783-A1.
 XX PD 27-JUL-1995.
 XX PF 25-JAN-1995; 95WO-US001000.
 XX PR 25-JAN-1994; 94US-00186266.
 XX PA (CYTE-) CYTEL CORP.
 XX FI Kubo RT, Grey HM, Sette A, Celis E;
 XX DR WPI; 1995-269270/35.
 XX PT Immunogenic peptide(s) that induce immune response to cancer cells - that
 XX PT express a MAGE-3 protein peptide epitope used in vaccines or adoptive
 XX PT immunotherapy to induce cytotoxic T lymphocytes.
 XX PS Disclosure; Page 14; 44pp; English.
 XX CC AAR75942 is derived from the sequence of the melanoma antigen (MAGE-3)
 CC protein and can be used to elicit a primary cytotoxic T lymphocyte
 CC response against cells expressing MAGE-3. Synthetic peptides AAR75945-53
 CC can be used therapeutically to elicit CTL responses to melanoma, breast,
 CC colon, prostate, or other cells which express proteins with this epitope.
 CC The peptides have specific HLA-A1 binding capacity. The peptides can be
 CC also used in vaccines, esp. combined with peptides such as AAR75955-56,
 CC which are T-helper epitopes
 XX SQ Sequence 21 AA;
 Query Match 52.7%; Score 89; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 2.1e-06;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 2 EKTIKMEKASSVFNVNS 20
 DB 3 EKTIKMEKASSVFNVNS 21
 RESULT 11
 AAR70912
 ID AAR70912 standard; protein; 21 AA.
 XX AC AAR70912;
 XX DT 27-AUG-2003 (revised)
 XX DT 25-MAR-2003 (revised)
 XX DT 09-OCT-1995 (first entry)
 XX DE Malaria circumsporozoite 378-398 T helper peptide.
 XX KW Human melanoma antigen; MAGE-1; vaccines; MAGE associated tumours;
 XX KW malaria circumsporozoite 378-398; T helper peptide.
 XX OS Plasmodium falciparum.
 XX PN WO9504542-A1.
 XX PD 16-FEB-1995.

XX 02-AUG-1994; 94WO-US008721.
 XX 06-AUG-1993; 93US-00103623.
 XX PA (CYTE-) CYTEL CORP.
 XX FI Fikes JD, Livingston BD, Sette AD, Sidney JC;
 XX DR WPI; 1995-090681/12.
 XX PT Human melanoma antigen, MAGE-1, peptide(s) - useful for stimulating
 XX PT immune response against melanoma.
 XX PS Disclosure; Page 13; 59pp; English.
 XX CC The T helper peptides described in AAR70910-R70914 are used in
 CC conjunction with the C-terminal MAGE-1 peptides described in AAR70915 to
 CC AAR70969. Compsns. containing the T helper and MAGE-1 peptides can be
 CC administered, as a vaccine to patients susceptible to MAGE associated
 CC tumors, e.g. melanomas. (Updated on 25-MAR-2003 to correct PN field.)
 XX CC (Updated on 27-AUG-2003 to correct OS field.)
 XX SQ Sequence 21 AA;
 Query Match 52.7%; Score 89; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 2.1e-06;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 2 EKTIKMEKASSVFNVNS 20
 DB 3 EKTIKMEKASSVFNVNS 21
 RESULT 12
 AAR82586
 ID AAR82586 standard; peptide; 21 AA.
 XX AC AAR82586;
 XX DT 13-JUN-1996 (first entry)
 XX DE Plasmodium falciparum circumsporozoite helper T cell epitope, PF.
 XX KW IGE; CH4; immunoglobulin; epsilon; immunogen; helper T cell; epitope;
 XX KW vaccine; allergy; antibody; constant heavy chain.
 XX OS Plasmodium falciparum.
 XX PN WO9526365-A1.
 XX PD 05-OCT-1995.
 XX PF 24-MAR-1995; 95WO-US003741.
 XX PR 28-MAR-1994; 94US-00218461.
 XX PR 25-OCT-1994; 94US-00328912.
 XX PA (UNBI-) UNITED BIOMEDICAL INC.
 XX PI Wang CY;
 XX DR WPI; 1995-351297/45.
 XX PT Synthetic peptide-based immunogen contg. IGE CH4 peptide and helper T
 XX PT cell epitope - useful for eliciting antibody prodn. for allergy
 XX PT treatment.
 XX PS Claim 3; Page 23; 87pp; English.
 XX CC AAR82571-91 are helper T cell epitopes which can be used in the
 CC preparation of a peptide immunogen that is useful in vaccines for
 CC treating allergic reactions. In the immunogen an IGE CH4 peptide is

CC attached C-terminally to a series of amino acids including a helper T
 CC cell epitope. The immunogen may also opt. contain a fatty acid or fatty
 CC acid derivative, an invasins domain or alpha-NH2. The immunogen produces
 CC high titres of antibodies to the effector site in human IGE heavy chain
 CC (the CH4 domain peptide) which inhibit mast cell activation and reduce
 CC allergen-induced IGE prodn. The immunogens may be used in either a
 CC radially branching multimeric form or a linearly arranged monomeric form
 XX
 XX Sequence 21 AA;

Query Match 52.7%; Score 89; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 2.1e-06;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EKXIAKMEKASSVFNVNS 20
 |||||
 DB 3 EKXIAKMEKASSVFNVNS 21

RESULT 13
 AAW05612
 ID AAW05612 standard; peptide; 21 AA.

XX AC AAW05612;

DT 10-DEC-1996 (first entry)

DE Circumsporozoite helper T cell epitope.

XX Immunoglobulin; IgE; membrane protein; human; epsilon chain; hepatitis B;
 KW membrane anchoring domain; helper T cell; surface antigen; core antigen;
 KW pertussis toxin; tetanus toxin; measles virus F protein; immunotherapy;
 KW Chlamydia trachomatis major outer membrane protein; immunogen; vaccine;
 KW diptheria toxin; Plasmodium falciparum; circumsporozoite; E. coli Tral;
 KW schistosoma mansoni; triose phosphate isomerase; allergenic reaction;
 KW allergic rhinitis; food allergy; anaphylaxis; virally-induced asthma;
 KW antihistamine; decongestant; beta-2 agonist; immunosuppression;
 KW corticosteroid.

XX Plasmodium falciparum.

XX WO9612740-A1.

PN 02-MAY-1996.

XX 25-OCT-1995; 95WO-US013841.

XX 25-OCT-1994; 94US-00328519.

XX (UNBI-) UNITED BIOMEDICAL INC.

XX Wang CY, Walfield AM;

XX WPI; 1996-230555/23.

XX Peptide immunogen useful in treatment of allergy - comprises membrane-
 PT bound IGE epsilon-chain peptide synthesised linearly in tandem with T
 PT helper epitope peptide.

XX Claim 2; Page 19; 53pp; English.

XX AAW05957-W05616 represent helper T cell epitopes used in the peptide
 CC immunogens of the invention. This sequence represents the Plasmodium
 CC falciparum circumsporozoite helper T cell antigen. The peptides of the
 CC invention contain one of these sequences, and a membrane-bound
 CC immunoglobulin E (IGE) fragment (see AAW05595 and AAW05596). The peptide
 CC immunogens of the invention can be used in vaccines for the
 CC immunotherapeutic treatment of allergenic reactions, including allergic
 CC rhinitis, food allergies, anaphylaxis, or virally-induced asthma. The
 CC immunogens overcome the short effective period of antihistamines,
 CC decongestants, and beta-2 agonists, while preventing the broad
 CC immunosuppression of corticosteroids. The peptides do not have the
 CC potential side effects of restlessness or sedation (associated with

CC antihistamines), associated increased morbidity in asthmatics (as seen
 CC with beta-2 agonists) and adverse hormonal activities (observed in
 CC corticosteroid users)

XX Sequence 21 AA;

Query Match 52.7%; Score 89; DB 2; Length 21;
 Best Local Similarity 100.0%; Pred. No. 2.1e-06;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EKXIAKMEKASSVFNVNS 20
 |||||
 DB 3 EKXIAKMEKASSVFNVNS 21

RESULT 14

AAW35440

ID AAW35440 standard; peptide; 21 AA.

XX AC AAW35440;

XX 25-MAR-2003 (revised)

DT 22-APR-1998 (first entry)

DE T-cell stimulatory peptide from Plasmodium falciparum.

XX T-cell stimulatory peptide; immunogen; non-dendritic; carrier; tumour;
 KW scaffold; inhibition; metastasis; wound healing; solid phase.

XX Plasmodium falciparum.

XX WO9738011-A1.

PD 16-OCT-1997.

XX 03-APR-1997; 97WO-DK000145.

XX 03-APR-1996; 96DK-00000398.

XX (PEPR-) PEPRESEARCH AS.

XX Heegaard PMH, Jakobsen PH;

XX WPI; 1997-512645/47.

XX Non-dendritic peptide carrier linked to a solid phase - useful as a
 PT diagnostic agent and as a scaffold for production of chemical
 PT derivatives.

XX Claim 30; Page 199; 262pp; English.

XX A non-dendritic peptide carrier (A) has been developed which is coupled
 CC through a linker to a solid phase, forming a complex of (A)-solid phase.
 CC Where (A) comprises 10-50 amino acids capable of forming a secondary
 CC structure in a benign buffer after liberation from the solid phase, and
 CC further the (A)-solid phase complex comprises an immunogenic substance
 CC and/or an immune mediator coupled on (A). The present sequence represents
 CC a specifically claimed T-cell stimulatory peptide from the present
 CC invention. An (A)-solid phase complex can be used as a scaffold for the
 CC production of chemical derivatives, characterised by covalently attaching
 CC molecules at attachment points. Alternatively (A) is used as a scaffold-
 CC peptide for the incorporation into an immunostimulating complex (Iscom)
 CC resulting an (A)-Iscom complex which is used for the chemical coupling of
 CC antigenic substances in an aqueous solution by conjugation. (A)
 CC derivatised with one or more peptides having fibronectin-, laminin- or
 CC vitronectin-like binding activities can be used for the promotion of cell
 CC attachment to plastic surfaces, in particular to inhibit tumour growth
 CC and metastasis, and for promotion of wound healing. Also a derivatised
 CC (A) can be used for the selection of specifically-binding aptamers or as
 CC a diagnostic agent. Such diagnostic-(A) molecules could be used to detect
 CC molecules derived from or indicative of pregnancy or of a disease, such
 CC as an infectious, autoimmune or cancerous disease. (Updated on 25-MAR-
 CC 2003 to correct PF field.)

```

XX SQ Sequence 21 AA;
Query Match 52.7%; Score 89; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.1e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EKXIAMEKASSVFNVVNS 20
Db 3 EKXIAMEKASSVFNVVNS 21

RESULT 15
AAV23252
ID AAY23252 standard; peptide; 21 AA.
XX AC AAY23252;
XX DT 31-AUG-1999 (first entry)
XX DE Peptide derived from Plasmodium falciparum CS protein.
XX KW Venezuelan equine encephalitis virus; VEE virus; neoplastic disease;
XX KW tumour-associated antigen; cytokine; immunity; cancer; tumour;
XX KW CS protein.
XX OS Plasmodium falciparum.
XX PN WO9930734-A1.
XX PD 24-JUN-1999.
XX PF 14-DEC-1998; 98WO-US025725.
XX PR 18-DEC-1997; 97US-0068080P.
XX PA (SEAR ) SEARLE & CO G D.
XX PI Hippenmeyer PJ;
XX DR WPI; 1999-395093/33.
XX PT Using new Venezuelan equine encephalitis virus vectors.
XX PS Claim 5; Page 24; 40pp; English.
XX CC The specification describes Venezuelan equine encephalitis (VEE) virus
CC vectors which can be used to express tumour-associated antigens and
CC cytokines, and thus induce immunity to cancer. The VEE virus vectors of
CC the invention can be used to prevent, treat, and protect against primary and
CC metastatic neoplastic diseases, especially tumours such as lung cancer,
CC breast cancer, ovarian cancer, prostate cancer, pancreatic cancer,
CC gastric cancer, colon cancer, renal cancer, bladder cancer, melanoma,
CC hepatoma, sarcoma and lymphoma. The present sequence is derived from the
CC Plasmodium falciparum CS protein, and can be fused with the target
CC peptide of the invention to provide a greater stimulation of the immune
CC system
XX SQ Sequence 21 AA;
Query Match 52.7%; Score 89; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.1e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 EKXIAMEKASSVFNVVNS 20
Db 3 EKXIAMEKASSVFNVVNS 21

Search completed: March 10, 2004, 09:12:11
Job time : 50.6926 secs

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OM protein - protein search, using sw model

Run on: March 10, 2004, 08:58:54 ; Search time 32.6148 Seconds
(without alignments)
319.245 Million cell updates/sec

Title: US-09-848-834A-12
Perfect score: 169
Sequence: 1 DEKIAKMEKASSVFNVNSGSLHWSYGLRPX 33

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL 25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	82	48.5	69	5 Q8MZK7	Q8MZK7 plasmodium
2	82	48.5	115	5 Q25837	Q25837 plasmodium
3	82	48.5	115	5 Q25839	Q25839 plasmodium
4	82	48.5	115	5 Q9U934	Q9U934 plasmodium
5	82	48.5	115	5 Q25835	Q25835 plasmodium
6	82	48.5	115	5 Q25836	Q25836 plasmodium
7	82	48.5	115	5 Q9U9V7	Q9U9V7 plasmodium
8	82	48.5	117	5 Q25795	Q25795 plasmodium
9	82	48.5	117	5 Q25796	Q25796 plasmodium
10	82	48.5	117	5 Q25797	Q25797 plasmodium
11	82	48.5	117	5 Q25794	Q25794 plasmodium
12	82	48.5	356	5 Q819G5	Q819G5 plasmodium
13	82	48.5	360	5 Q819H7	Q819H7 plasmodium
14	82	48.5	360	5 Q819H6	Q819H6 plasmodium
15	82	48.5	363	5 Q819H3	Q819H3 plasmodium
16	82	48.5	364	5 Q819G4	Q819G4 plasmodium

17	82	48.5	368	5 Q819G3	Q819G3 plasmodium
18	82	48.5	380	5 Q819G8	Q819G8 plasmodium
19	82	48.5	380	5 Q819G1	Q819G1 plasmodium
20	82	48.5	385	5 Q819I9	Q819I9 plasmodium
21	82	48.5	385	5 Q819I8	Q819I8 plasmodium
22	82	48.5	388	5 Q819H4	Q819H4 plasmodium
23	82	48.5	389	5 Q819J2	Q819J2 plasmodium
24	82	48.5	389	5 Q81056	Q81056 plasmodium
25	82	48.5	392	5 Q819H8	Q819H8 plasmodium
26	82	48.5	392	5 Q819H1	Q819H1 plasmodium
27	82	48.5	392	5 Q819H0	Q819H0 plasmodium
28	82	48.5	392	5 Q819G2	Q819G2 plasmodium
29	82	48.5	393	5 Q819J1	Q819J1 plasmodium
30	82	48.5	393	5 Q819J0	Q819J0 plasmodium
31	82	48.5	396	5 Q819I1	Q819I1 plasmodium
32	82	48.5	396	5 Q819I0	Q819I0 plasmodium
33	82	48.5	396	5 Q819H9	Q819H9 plasmodium
34	82	48.5	397	5 Q819I7	Q819I7 plasmodium
35	82	48.5	397	5 Q819I6	Q819I6 plasmodium
36	82	48.5	404	5 Q819I5	Q819I5 plasmodium
37	82	48.5	408	5 Q25729	Q25729 plasmodium
38	82	48.5	408	5 Q819G9	Q819G9 plasmodium
39	82	48.5	408	5 Q810I0	Q810I0 plasmodium
40	82	48.5	412	5 Q819I4	Q819I4 plasmodium
41	82	48.5	412	5 Q819H5	Q819H5 plasmodium
42	82	48.5	412	5 Q819H2	Q819H2 plasmodium
43	82	48.5	412	5 Q819G7	Q819G7 plasmodium
44	82	48.5	412	5 Q819G5	Q819G5 plasmodium
45	82	48.5	412	5 Q810R5	Q810R5 plasmodium

ALIGNMENTS

RESULT 1
Q8MZK7 PRELIMINARY; PRT; 69 AA.

AC Q8MZK7; 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Circumsporozoite protein II (Fragment).
GN CSPII.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FC1/HN;
RA Chen H.H., Yu X.B., Wu Z.D., Xu J.;
RT "Gene cloning of circumsporozoite protein (CSP) II gene from
RT Plasmodium falciparum (FC1/HN).";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY093672; AAM19072.1; -
DR GO; GO:0003793; F:defense/immunity protein activity; IBA.
DR InterPro; IPR0003067; Circmsprzoite.
DR InterPro; IPR000884; TSPI.
DR Pfam; PF00090; tsd.1; 1.
DR PRINTS; PRO3303; CRCMSPRZOITE.
DR SMART; SM00209; TSPI; 1.
DR PROSITE; PS00992; TSPI; 1.
FT NON TER 1 1
SQ SEQUENCE 69 AA; 7670 MW; F3E1AA54671FE6FF CRC64;

Query Match 48.5%; Score 82; DB 5; Length 69;
Best Local Similarity 78.3%; Pred No. 0.00028;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 EKIAKMEKASSVFNVNSGSL 24
Db 37 EKICKMEKCKSSVFNVNSIGL 59

```

RESULT 2
Q25837      PRELIMINARY;      PRT; 115 AA.
AC Q25837;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Circumsporozoite protein (Fragment).
GN CSP.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=835a;
RX MEDLINE=95077069; PubMed=7985759;
RA Jongwutiwes S., Tanabe K., Hughes M.K., Kanbara H., Hughes A.L.;
RT "Allelic variation in the circumsporozoite protein of Plasmodium
RT falciparum from Thai field isolates.";
RL Am. J. Trop. Med. Hyg. 51:659-668(1994).
DR EMBL; M83160; AAA29573.1; -
DR GO; GO:0003793; F:defense/immunity protein activity; IEA.
DR InterPro; IPR003067; Crmsprzoite.
DR Pfam; PF00090; tsp.1; 1.
DR PRINTS; PR01303; CRMSPRZOITE.
DR SMART; SM00209; TSPI; 1.
DR PROSITE; PS50092; TSPI; 1.
FT NON TER 1
SQ SEQUENCE 115 AA; 13018 MW; COA23F5805688237 CRC64;

Query Match 48.5%; Score 82; DB 5; Length 115;
Best Local Similarity 78.3%; Pred. No. 0.00049;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 EKKIAKMEKASSVFVNVSIGL 24
Db 83 EKKICKMEKCSVFVNVSIGL 105

RESULT 3
Q25839      PRELIMINARY;      PRT; 115 AA.
AC Q25839;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Circumsporozoite protein (Fragment).
GN CSP.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=835c;
RX MEDLINE=95077069; PubMed=7985759;
RA Jongwutiwes S., Tanabe K., Hughes M.K., Kanbara H., Hughes A.L.;
RT "Allelic variation in the circumsporozoite protein of Plasmodium
RT falciparum from Thai field isolates.";
RL Am. J. Trop. Med. Hyg. 51:659-668(1994).
DR EMBL; M83162; AAA29575.1; -
DR GO; GO:0003793; F:defense/immunity protein activity; IEA.
DR InterPro; IPR003067; Crmsprzoite.
DR Pfam; PF00090; tsp.1; 1.
DR PRINTS; PR01303; CRMSPRZOITE.
DR SMART; SM00209; TSPI; 1.
DR PROSITE; PS50092; TSPI; 1.
FT NON TER 1
SQ SEQUENCE 115 AA; 12974 MW; 6B5538287260DA90 CRC64;

Query Match 48.5%; Score 82; DB 5; Length 115;
Best Local Similarity 78.3%; Pred. No. 0.00049;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 EKKIAKMEKASSVFVNVSIGL 24
Db 83 EKKICKMEKCSVFVNVSIGL 105

RESULT 4
Q25834      PRELIMINARY;      PRT; 115 AA.
AC Q25834;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Circumsporozoite protein (Fragment).
GN CSP.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=822a;
RX MEDLINE=95077069; PubMed=7985759;
RA Jongwutiwes S., Tanabe K., Hughes M.K., Kanbara H., Hughes A.L.;
RT "Allelic variation in the circumsporozoite protein of Plasmodium
RT falciparum from Thai field isolates.";
RL Am. J. Trop. Med. Hyg. 51:659-668(1994).
DR EMBL; M83154; AAA29567.1; -
DR GO; GO:0003793; F:defense/immunity protein activity; IEA.
DR InterPro; IPR003067; Crmsprzoite.
DR Pfam; PF00090; tsp.1; 1.
DR PRINTS; PR01303; CRMSPRZOITE.
DR SMART; SM00209; TSPI; 1.
DR PROSITE; PS50092; TSPI; 1.
FT NON TER 1
SQ SEQUENCE 115 AA; 12925 MW; A24CB33ABE3F232 CRC64;

Query Match 48.5%; Score 82; DB 5; Length 115;
Best Local Similarity 78.3%; Pred. No. 0.00049;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 EKKIAKMEKASSVFVNVSIGL 24
Db 83 EKKICKMEKCSVFVNVSIGL 105

RESULT 5
Q25835      PRELIMINARY;      PRT; 115 AA.
AC Q25835;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Circumsporozoite protein (Fragment).
GN CSP.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=828;
RX MEDLINE=95077069; PubMed=7985759;
RA Jongwutiwes S., Tanabe K., Hughes M.K., Kanbara H., Hughes A.L.;
RT "Allelic variation in the circumsporozoite protein of Plasmodium
RT falciparum from Thai field isolates.";
RL Am. J. Trop. Med. Hyg. 51:659-668(1994).
DR EMBL; M83157; AAA29570.1; -
DR GO; GO:0003793; F:defense/immunity protein activity; IEA.
DR InterPro; IPR003067; Crmsprzoite.
DR Pfam; PF00090; tsp.1; 1.
DR PRINTS; PR01303; CRMSPRZOITE.

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DR SMART; SM00209; TSP1; 1.
DR PROSITE; PS50092; TSP1; 1.
FT NON_TER 1
SQ SEQUENCE 115 AA; 12925 MW; 9BES2CPFF12BD48F CRC64;

Query Match
Best Local Similarity 48.5%; Score 82; DB 5; Length 115;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 EKKIAKMEKASSVFNVNNSIGL 24
Db 83 EKKICKMEKCSSVFNVNNSIGL 105

RESULT 6
Q25836 PRELIMINARY; PRT; 115 AA.
AC Q25836
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Circumsporozoite protein (Fragment).
GN CSP.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=834b;
RA Jongsutwises S., Tanabe K., Hughes M.K., Kanbara H., Hughes A.L.;
RT "Allelic variation in the circumsporozoite protein of Plasmodium falciparum from Thai field isolates."
RL Am. J. Trop. Med. Hyg. 51:659-668(1994).
DR EMBL; M83159; AAA29572.1; -.
DR InterPro; IPR003067; Crcmsprzoite.
DR GO; GO:0003793; F:defense/immunity protein activity; IEA.
DR SMART; SM00209; TSP1; 1.
DR PROSITE; PS50092; TSP1; 1.
FT NON_TER 1
SQ SEQUENCE 115 AA; 12926 MW; 697DF630E50B3A30 CRC64;

Query Match
Best Local Similarity 48.5%; Score 82; DB 5; Length 115;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 EKKIAKMEKASSVFNVNNSIGL 24
Db 83 EKKICKMEKCSSVFNVNNSIGL 105

RESULT 7
Q25796 PRELIMINARY; PRT; 115 AA.
AC Q25796
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Circumsporozoite protein (Fragment).
GN CSP.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=815, 947, and 808;
RA Jongsutwises S., Tanabe K., Hughes M.K., Kanbara H., Hughes A.L.;
RT "Allelic variation in the circumsporozoite protein of Plasmodium falciparum from Thai field isolates."

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RL Am. J. Trop. Med. Hyg. 51:659-668(1994).
DR EMBL; M83153; AAA29566.1; -.
DR EMBL; M83171; AAA29549.1; -.
DR EMBL; M83151; AAA29564.1; -.
DR GO; GO:0003793; F:defense/immunity protein activity; IEA.
DR InterPro; IPR003067; Crcmsprzoite.
DR InterPro; IPR000884; TSP1.
DR Pfam; PF00090; tsp.1; 1.
DR PRINTS; PR01303; CRCMSPRZOITE.
DR SMART; SM00209; TSP1; 1.
DR PROSITE; PS50092; TSP1; 1.
FT NON_TER 1
SQ SEQUENCE 115 AA; 12925 MW; 697DF63EBBBD490 CRC64;

Query Match
Best Local Similarity 48.5%; Score 82; DB 5; Length 115;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 EKKIAKMEKASSVFNVNNSIGL 24
Db 83 EKKICKMEKCSSVFNVNNSIGL 105

RESULT 8
Q25795 PRELIMINARY; PRT; 117 AA.
AC Q25795
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Circumsporozoite protein (Fragment).
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RA Doolan D.L., Saul A., Good M.F.;
RT "Geographically restricted heterogeneity of the Plasmodium falciparum circumsporozoite protein: relevance for vaccine development.";
RL Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.
DR EMBL; M77203; AAA29517.2; -.
DR GO; GO:0003793; F:defense/immunity protein activity; IEA.
DR InterPro; IPR003067; Crcmsprzoite.
DR InterPro; IPR000884; TSP1.
DR Pfam; PF00090; tsp.1; 1.
DR PRINTS; PR01303; CRCMSPRZOITE.
DR SMART; SM00209; TSP1; 1.
DR PROSITE; PS50092; TSP1; 1.
FT NON_TER 1
SQ SEQUENCE 117 AA; 13110 MW; D96BE20944A7C726 CRC64;

Query Match
Best Local Similarity 48.5%; Score 82; DB 5; Length 117;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 EKKIAKMEKASSVFNVNNSIGL 24
Db 85 EKKICKMEKCSSVFNVNNSIGL 107

RESULT 9
Q25796 PRELIMINARY; PRT; 117 AA.
AC Q25796
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Circumsporozoite protein (Fragment).
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]

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RP SEQUENCE FROM N.A.
RA Doonan D.L., Saul A., Good M.F.;
RT "Geographically restricted heterogeneity of the Plasmodium falciparum
RT Circumsporozoite protein: relevance for vaccine development.";
RL Submitted (FEB-1992) to the EMBL/GenBank/DBSJ databases.
DR EMBL; M77204; AAA29518.2; -.
DR GO; GO:0003793; F:defense/immunity protein activity; IEA.
DR InterPro; IPR003067; Circumsporozoite.
DR Pfam; PF00090; tsp.1; 1.
DR PRINTS; PR01303; CRCMSPRZOITE.
DR SMART; SM00209; TSPI; 1.
DR PROSITE; PS50092; TSPI; 1.
FT NON TER 1
FT NON TER 1
SQ SEQUENCE 117 AA; 13052 MW; D96BE209420BADE6 CRC64;

Query Match 48.5%; Score 82; DB 5; Length 117;
Best Local Similarity 78.3%; Pred. No. 0.0005; 5; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 EKKIAKMEKASSVFNVNNGPSL 24
DB 85 EKKICKMEKCSSVFNVNNGSIGL 107

RESULT 10
ID Q25797 PRELIMINARY; PRT; 117 AA.
AC Q25797;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Circumsporozoite protein (Fragment).
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
CX NCBI_TaxID=5833;
RN Doonan D.L., Saul A., Good M.F.;
RA "Geographically restricted heterogeneity of the Plasmodium falciparum
RT Circumsporozoite protein: relevance for vaccine development.";
RL Submitted (FEB-1992) to the EMBL/GenBank/DBSJ databases.
DR EMBL; M77205; AAA29519.2; -.
DR GO; GO:0003793; F:defense/immunity protein activity; IEA.
DR InterPro; IPR003067; Circumsporozoite.
DR Pfam; PF00090; tsp.1; 1.
DR PRINTS; PR01303; CRCMSPRZOITE.
DR SMART; SM00209; TSPI; 1.
DR PROSITE; PS50092; TSPI; 1.
FT NON TER 1
FT NON TER 1
SQ SEQUENCE 117 AA; 13043 MW; ODA711D86C0B03C1 CRC64;

Query Match 48.5%; Score 82; DB 5; Length 117;
Best Local Similarity 78.3%; Pred. No. 0.0005; 5; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 EKKIAKMEKASSVFNVNNGPSL 24
DB 85 EKKICKMEKCSSVFNVNNGSIGL 107

RESULT 11
ID Q25794 PRELIMINARY; PRT; 117 AA.
AC Q25794;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Circumsporozoite protein (Fragment).
OS Plasmodium falciparum.

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OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN Doonan D.L., Saul A., Good M.F.;
RA "Geographically restricted heterogeneity of the Plasmodium falciparum
RT Circumsporozoite protein: relevance for vaccine development.";
RL Submitted (FEB-1992) to the EMBL/GenBank/DBSJ databases.
DR EMBL; M77202; AAA29516.2; -.
DR GO; GO:0003793; F:defense/immunity protein activity; IEA.
DR InterPro; IPR003067; Circumsporozoite.
DR Pfam; PF00090; tsp.1; 1.
DR PRINTS; PR01303; CRCMSPRZOITE.
DR SMART; SM00209; TSPI; 1.
DR PROSITE; PS50092; TSPI; 1.
FT NON TER 1
FT NON TER 1
SQ SEQUENCE 117 AA; 13080 MW; 8F9B92CC10ECC212 CRC64;

Query Match 48.5%; Score 82; DB 5; Length 117;
Best Local Similarity 78.3%; Pred. No. 0.0005; 5; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 EKKIAKMEKASSVFNVNNGPSL 24
DB 85 EKKICKMEKCSSVFNVNNGSIGL 107

RESULT 12
ID Q819G5 PRELIMINARY; PRT; 356 AA.
AC Q819G5;
DT 01-MAR-2003 (T-EMBLrel. 23, Created)
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Circumsporozoite protein.
GN CSP.
OS Plasmodium falciparum (isolate fid3 / India).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=70152;
RN Doonan D.L., Saul A., Good M.F.;
RA "Geographically restricted heterogeneity of the Plasmodium falciparum
RT Circumsporozoite protein: relevance for vaccine development.";
RL Submitted (FEB-1992) to the EMBL/GenBank/DBSJ databases.
DR EMBL; M77205; AAA29519.2; -.
DR GO; GO:0003793; F:defense/immunity protein activity; IEA.
DR InterPro; IPR003067; Circumsporozoite.
DR Pfam; PF00090; tsp.1; 1.
DR PRINTS; PR01303; CRCMSPRZOITE.
DR SMART; SM00209; TSPI; 1.
DR PROSITE; PS50092; TSPI; 1.
SQ SEQUENCE 356 AA; 38840 MW; B1AB87D66609A100 CRC64;

Query Match 48.5%; Score 82; DB 5; Length 356;
Best Local Similarity 78.3%; Pred. No. 0.0017; 5; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 EKKIAKMEKASSVFNVNNGPSL 24
DB 324 EKKICKMEKCSSVFNVNNGSIGL 346

RESULT 13
ID Q819H7 PRELIMINARY; PRT; 360 AA.
AC Q819H7;

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DT 01-MAR-2003 (TREMELrel. 23, Created)
 DT 01-MAR-2003 (TREMELrel. 23, Last sequence update)
 DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
 DE Circumsporozoite protein.
 CSP.
 OS Plasmodium falciparum.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5833;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Asemo Bay;
 RX MEDLINE=22356746; PubMed=12467976;
 RA Escalante A.A., Grebert H.M., Isea R., Goldman I.F., Basco L.,
 RA Magris M., Biswas S., Kariuki S., Lal A.A.;
 RT "A study of genetic diversity in the gene encoding the
 RT circumsporozoite protein (CSP) of Plasmodium falciparum from different
 RT transmission areas-XVI. Asemo Bay Cohort Project.";
 RL Mol. Biochem. Parasitol. 125:83-90(2002).
 DR EMBL; AF540462; AAN87596.1; -
 DR GO; GO:0003793; F:defense/immunity protein activity; IEA.
 DR InterPro; IPR003067; Crcmsprzoite.
 DR Pfam; PF00090; tsp.1; 1.
 DR PRINTS; PR01303; CRCMSPRZOITE.
 DR SMART; SM00209; TSP1; 1.
 DR PROSITE; PS50092; TSP1; 1.
 SQ SEQUENCE 360 AA; 39093 MW; 6504CC012649236C CRC64;

Query Match 48.5%; Score 82; DB 5; Length 360;
 Best Local Similarity 78.3%; Pred. No. 0.0018; 5; Indels 0; Gaps 0;
 Matches 18; Conservative 0; Mismatches 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 EKXIAKMEKASSVFNVNSGPSL 24
 |||||
 Db 328 EKXICKMEKCSSVFNVNSIGL 350

RESULT 14

Q819H6 PRELIMINARY; PRT; 360 AA.
 AC Q819H6;
 DT 01-MAR-2003 (TREMELrel. 23, Created)
 DT 01-MAR-2003 (TREMELrel. 23, Last sequence update)
 DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
 DE Circumsporozoite protein.
 CSP.
 OS Plasmodium falciparum.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5833;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Asemo Bay;
 RX MEDLINE=22356746; PubMed=12467976;
 RA Escalante A.A., Grebert H.M., Isea R., Goldman I.F., Basco L.,
 RA Magris M., Biswas S., Kariuki S., Lal A.A.;
 RT "A study of genetic diversity in the gene encoding the
 RT circumsporozoite protein (CSP) of Plasmodium falciparum from different
 RT transmission areas-XVI. Asemo Bay Cohort Project.";
 RL Mol. Biochem. Parasitol. 125:83-90(2002).
 DR EMBL; AF540463; AAN87597.1; -
 DR GO; GO:0003793; F:defense/immunity protein activity; IEA.
 DR InterPro; IPR003067; Crcmsprzoite.
 DR Pfam; PF00090; tsp.1; 1.
 DR PRINTS; PR01303; CRCMSPRZOITE.
 DR SMART; SM00209; TSP1; 1.
 DR PROSITE; PS50092; TSP1; 1.
 SQ SEQUENCE 360 AA; 39062 MW; 65058844270D666C CRC64;

Query Match 48.5%; Score 82; DB 5; Length 360;
 Best Local Similarity 78.3%; Pred. No. 0.0018;
 Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 EKXIAKMEKASSVFNVNSGPSL 24
 |||||
 Db 328 EKXICKMEKCSSVFNVNSIGL 350

RESULT 15

Q819H3 PRELIMINARY; PRT; 363 AA.
 AC Q819H3;
 DT 01-MAR-2003 (TREMELrel. 23, Created)
 DT 01-MAR-2003 (TREMELrel. 23, Last sequence update)
 DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
 DE Circumsporozoite protein.
 CSP.
 OS Plasmodium falciparum.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5833;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Boliviar;
 RX MEDLINE=22356746; PubMed=12467976;
 RA Escalante A.A., Grebert H.M., Isea R., Goldman I.F., Basco L.,
 RA Magris M., Biswas S., Kariuki S., Lal A.A.;
 RT "A study of genetic diversity in the gene encoding the
 RT circumsporozoite protein (CSP) of Plasmodium falciparum from different
 RT transmission areas-XVI. Asemo Bay Cohort Project.";
 RL Mol. Biochem. Parasitol. 125:83-90(2002).
 DR EMBL; AF540466; AAN87600.1; -
 DR GO; GO:0003793; F:defense/immunity protein activity; IEA.
 DR InterPro; IPR003067; Crcmsprzoite.
 DR Pfam; PF00090; tsp.1; 1.
 DR PRINTS; PR01303; CRCMSPRZOITE.
 DR SMART; SM00209; TSP1; 1.
 DR PROSITE; PS50092; TSP1; 1.
 SQ SEQUENCE 363 AA; 39458 MW; E88E17AC5A11BD55 CRC64;

Query Match 48.5%; Score 82; DB 5; Length 363;
 Best Local Similarity 78.3%; Pred. No. 0.0018;
 Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 EKXIAKMEKASSVFNVNSGPSL 24
 |||||
 Db 331 EKXICKMEKCSSVFNVNSIGL 353

Search completed: March 10, 2004, 09:25:35
 Job time : 33.6148 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 10, 2004, 08:58:53 ; Search time 6.03502 Seconds
(without alignments)
284.724 Million cell updates/sec

Title: US-09-848-834A-12
Perfect score: 169
Sequence: 1 DEKXIAOMKASSVFNVNSGSLHWSYGLRXP 33

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	82	48.5	388	1 CSP_PLARE	P26694 Plasmodium
2	82	48.5	397	1 CSP_PLAFO	P19597 Plasmodium
3	82	48.5	412	1 CSP_PLAFA	P02893 Plasmodium
4	82	48.5	424	1 CSP_PLAFT	P13814 Plasmodium
5	82	48.5	442	1 CSP_PLAFW	P08307 Plasmodium
6	56.5	33.4	92	1 GON1_RAT	P07490 rattus norv
7	55	32.5	339	1 CSP_PLABE	P06915 Plasmodium
8	55	32.5	347	1 CSP_PLABA	P23093 Plasmodium
9	55	32.5	367	1 CSP_PLAYO	P05914 Plasmodium
10	54	32.0	67	1 GON1_MACMU	P55247 macaca mula
11	54	32.0	90	1 GON1_MOUSE	P13562 mus musculus
12	54	32.0	91	1 GON1_PIG	P49921 sus scrofa
13	54	32.0	92	1 GON1_HUMAN	P01148 homo sapien
14	54	32.0	95	1 GON1_PAGMA	P70074 pagrus majo
15	52	30.8	61	1 GON1_SHEEP	Q28588 ovis aries
16	52	30.8	63	1 GON1_VESAU	O09163 mesocricetu
17	52	30.8	89	1 GON1_XENLA	P45656 xenopus lae
18	52	30.8	90	1 GON1_RANCA	Q90y63 rana catesb
19	52	30.8	92	1 GON1_TUPGB	Q95335 tupia glis
20	52	30.8	994	1 DPO2_KULJA	P05468 kluyveromyc
21	51	30.2	91	1 GON1_ORYLA	Q9dgc8 o prognado
22	51	30.2	92	1 GON1_CAVPO	O54713 cavia porce
23	51	30.2	393	1 CSP_PLABR	P14593 Plasmodium
24	51	30.2	429	1 CSP_PLAWA	P13815 Plasmodium
25	51	30.2	473	1 SYE_WIGBR	Q8C375 wiggleswort
26	50	29.6	95	1 GON1_SPAAU	P51919 sparus aura
27	50	29.6	2339	1 RPI1_PLAFA	P27625 Plasmodium
28	49.5	29.3	630	1 ESA8_TRYBB	P23799 trypanosoma
29	49.5	29.3	3176	1 CA36_HUMAN	P12111 homo sapien
30	49	29.0	95	1 GON1_WORSA	O73812 morone saxa
31	49	29.0	532	1 INV4_YEAST	P10596 saccharomyc
32	49	29.0	1146	1 ITAL_DROME	Q24247 drosophila
33	48.5	28.7	630	1 ESA8_TRYEQ	P26337 trypanosoma

ALIGNMENTS

RESULT 1

ID	CSP_PLARE	STANDARD;	PRT;	388 AA.
AC	P26694;			
DT	01-AUG-1992 (Rel. 23, Created)			
DT	01-AUG-1992 (Rel. 23, Last sequence update)			
DT	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	Circumsporozoite protein precursor (CS).			
OS	Plasmodium reichenowi.			
OC	Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.			
OX	NCBI_TaxID:5854;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE:91201303; PubMed:2016283;			
RA	Lal A.A., Goldman I.F.;			
RT	"Circumsporozoite protein gene from Plasmodium reichenowi, a chimpanzee malaria parasite evolutionarily related to the human malaria parasite Plasmodium falciparum.";			
RL	J. Biol. Chem. 266:6886-6889(1991).			
CC	-!- FUNCTION: The circumsporozoite protein is the immunodominant surface antigen on the sporozoite (the infective stage of the malaria parasite that is transmitted from the mosquito to the vertebrate host).			
CC	-!- MISCELLANEOUS: The C-terminal region is probably used for anchoring the protein to the cell membrane. The repeat sequences would be the surface antigen of the organism.			
CC	-!- SIMILARITY: Contains 1 TSP type-1 domain.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC	EMBL; M60972; AAA29561.1; -			
DR	PIR; A39756; A39756.			
DR	InterPro; IPR003067; Crcmsprzoite.			
DR	InterPro; IPR000884; TSP1.			
DR	Pfam; PF00090; tsp_1; 1.			
DR	PRINTS; PR01303; Crcmsprzoite.			
DR	SMART; SM00209; TSP1; 1.			
DR	PROSITE; PS00092; TSP1; 1.			
DR	Q9dgc8 o prognado			
KW	Malaria; Sporozoite; Repeat; Signal.			
FT	SIGNAL 1 16			
FT	CHAIN 17 388			
FT	DONAIN 120 263			
FT	REPEAT 120 123			
FT	REPEAT 124 127			
FT	REPEAT 128 131			
FT	REPEAT 132 135			
FT	REPEAT 136 139			
FT	REPEAT 140 143			
FT	REPEAT 144 147			

CIRCUMSPOROZOITE PROTEIN.
37 X 4 AA TANDEM REPEATS OF N-[AV]-[ND]-P.


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FT REPEAT 148 151 8.
FT REPEAT 152 155 9.
FT REPEAT 156 159 10.
FT REPEAT 160 163 11.
FT REPEAT 164 167 12.
FT REPEAT 168 171 13.
FT REPEAT 172 175 14.
FT REPEAT 176 179 15.
FT REPEAT 180 183 16.
FT REPEAT 184 187 17.
FT REPEAT 188 191 18.
FT REPEAT 192 195 19.
FT REPEAT 196 199 20.
FT REPEAT 200 203 21.
FT REPEAT 204 207 22.
FT REPEAT 208 211 23.
FT REPEAT 212 215 24.
FT REPEAT 216 219 25.
FT REPEAT 220 223 26.
FT REPEAT 224 227 27.
FT REPEAT 228 231 28.
FT REPEAT 232 235 29.
FT REPEAT 236 239 30.
FT REPEAT 240 243 31.
FT REPEAT 244 247 32.
FT REPEAT 248 251 33.
FT REPEAT 252 255 34.
FT REPEAT 256 259 35.
FT REPEAT 260 263 36.
FT REPEAT 264 267 37.
FT DOMAIN 313 366 TSP TYPE-1.
SQ SEQUENCE 388 AA; 42245 MW; C031BEFBE235604 CRC64;

Query Match 48.5%; Score 82; DB 1; Length 388;
Best Local Similarity 78.3%; Pred. No. 0.00033;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Cy 2 EKXIAKMEKASSVFNVNNGPSL 24
Db 356 EKXIAKMEKASSVFNVNNGPSL 378

RESULT 2
CSP_PLAFO STANDARD; PRT; 397 AA.
ID P19597; Q25798;
AC 01-FEB-1991 (Rel. 17, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 15-MAR-2004 (Rel. 43, Last annotation update)
DE Circumsporozoite protein precursor (CS).
OS Plasmodium falciparum (isolate NF54).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5843;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89345189; PubMed=2668895;
RA Campbell J.R.;
RT "DNA sequence of the gene encoding a Plasmodium falciparum malaria
candidate vaccine antigen."
RL Nucleic Acids Res. 17:5854-5854 (1989).
RN [2]
RP REVISIONS.
RA Campbell J.R.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=92152598; PubMed=1346766;
RA Davis J.R., Cortese J.F., Harrington D.A., Murphy J.R., Clyde D.F.,
RA Thomas A.W., Baqar S., Cochran M.A., Thanassi J., Levine M.N.,
RA Hackett C.S.;
RT "Plasmodium falciparum: in vitro characterization and human
infectivity of a cloned line".
RL Exp. Parasitol. 74:159-168 (1992).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=8936498; PubMed=2671723;
RA Caspese P., Gentz R., Matile H., Pink J.R., Sinigaglia F.;
RT "The circumsporozoite protein gene from NF54, a Plasmodium falciparum
isolate used in malaria vaccine trials."
RL Mol. Biochem. Parasitol. 35:185-190 (1989).
CC -!- FUNCTION: The circumsporozoite protein is the immunodominant
surface antigen on the sporozoite (the infective stage of the
malaria parasite that is transmitted from the mosquito to the
vertebrate host).
CC -!- MISCELLANEOUS: The C-terminal region is probably used for
anchoring the protein to the cell membrane. The repeat sequences
would be the surface antigen of the organism.
CC -!- SIMILARITY: Contains 1 TSP type-1 domain.
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CC EMBL; X15363; CAA33421.1; -
DR EMBL; M83886; AAA29521.1; -
DR EMBL; M22982; AAA29527.1; -
DR PIR; S05428; S05428.
DR InterPro; IPR003067; Crcmsprzoite.
DR InterPro; IPR000884; TSP1.
DR Pfam; PF00090; tsp_1; 1.
DR PRINTS; PR01303; CRCMSPRZOITE.
DR SMART; SM00209; TSP1; 1.
DR PROSITE; PS50092; TSP1; 1.
KW Malaria; Sporozoite; Repeat; Signal.
FT SIGNAL 1 16
FT CHAIN 17 397
FT DOMAIN 105 272
FT REPEAT 105 108 1.
FT REPEAT 109 112 2.
FT REPEAT 113 116 3.
FT REPEAT 117 120 4.
FT REPEAT 121 124 5.
FT REPEAT 125 128 6.
FT REPEAT 129 132 7.
FT REPEAT 133 136 8.
FT REPEAT 137 140 9.
FT REPEAT 141 144 10.
FT REPEAT 145 148 11.
FT REPEAT 149 152 12.
FT REPEAT 153 156 13.
FT REPEAT 157 160 14.
FT REPEAT 161 164 15.
FT REPEAT 165 168 16.
FT REPEAT 169 172 17.
FT REPEAT 173 176 18.
FT REPEAT 177 180 19.
FT REPEAT 181 184 20.
FT REPEAT 185 188 21.
FT REPEAT 189 192 22.
FT REPEAT 193 196 23.
FT REPEAT 197 200 24.
FT REPEAT 201 204 25.
FT REPEAT 205 208 26.
FT REPEAT 209 212 27.
FT REPEAT 213 216 28.
FT REPEAT 217 220 29.
FT REPEAT 221 224 30.
FT REPEAT 225 228 31.
FT REPEAT 229 232 32.
FT REPEAT 233 236 33.
FT REPEAT 237 240 34.
FT REPEAT 241 244 35.

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FT REPEAT 245 248 36.
FT REPEAT 249 252 37.
FT REPEAT 253 256 38.
FT REPEAT 257 260 39.
FT REPEAT 261 264 40.
FT REPEAT 265 268 41.
FT REPEAT 269 272 42.
FT DOMAIN 322 375 TSP TYPE-1.
FT CONFLICT 194 194 A -> ANPNANFNA (IN REF. 4).
SQ SEQUENCE 397 AA; 42646 MW; 9E81146F59EBCEA3 CRC64;

Query Match 48.5%; Score 82; DB 1; Length 397;
Best Local Similarity 78.3%; Pred. No. 0.00034;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 EKXIARMEKASVFNVNNGPSL 24
Db 365 EKXICKMEKCSSVFNVNSSIGL 387

RESULT 3
CSP_PLAFA STANDARD; PRT; 412 AA.
AC P02893;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Circumsporozoite protein precursor (CS).
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID:5833;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84250215; PubMed=6204383;
RA Dame J.B., Williams J.L., McCutchan T.F., Weber J.L., Wirtz R.A.,
RA Hochmeyer W.T., Maloy W.L., Haynes J.D., Schneider I., Roberts D.,
RA Sanders G.S., Reddy E.P., Diggs C.L., Miller L.H.;
RT "Structure of the gene encoding the immunodominant surface antigen on
RT the sporozoite of the human malaria parasite Plasmodium falciparum.";
RL Science 225:593-599(1984)
CC -!- FUNCTION: The circumsporozoite protein is the immunodominant
CC surface antigen on the sporozoite (the infective stage of the
CC malaria parasite that is transmitted from the mosquito to the
CC vertebrate host).
CC -!- MISCELLANEOUS: The C-terminal region is probably used for
CC anchoring the protein to the cell membrane. The repeat sequences
CC would be the surface antigen of the organism.
CC -!- SIMILARITY: Contains 1 TSP type-1 domain.
CC
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CC
DR EMBL; K02194; AAA29524.1; -
DR PIR; A03388; OZZCAF.
DR InterPro; IPR003067; Crcmsprzoite.
DR InterPro; IPR000884; TSPI.
DR Pfam; PF00090; tps 1.1.
DR PRINTS; PR01303; CRCMSPRZOITE.
DR SMART; SM00209; TSPI; 1.
DR PROSITE; PS00092; TSPI; 1.
KW Malaria; Sporozoite; Repeat; Signal.
FT SIGNAL 1 16 PROBABLE.
FT CHAIN 17 412 CIRCUMSPOROZOITE PROTEIN.
FT DOMAIN 123 286 41 X 4 AA TANDEM REPEATS OF P-N-[AV]-
FT REPEAT 123 126 [ND].
FT REPEAT 127 130 2.
FT REPEAT 131 134 3.

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FT REPEAT 135 138 4.
FT REPEAT 139 142 5.
FT REPEAT 143 146 6.
FT REPEAT 147 150 7.
FT REPEAT 151 154 8.
FT REPEAT 155 158 9.
FT REPEAT 159 162 10.
FT REPEAT 163 166 11.
FT REPEAT 167 170 12.
FT REPEAT 171 174 13.
FT REPEAT 175 178 14.
FT REPEAT 179 182 15.
FT REPEAT 183 186 16.
FT REPEAT 187 190 17.
FT REPEAT 191 194 18.
FT REPEAT 195 198 19.
FT REPEAT 199 202 20.
FT REPEAT 203 206 21.
FT REPEAT 207 210 22.
FT REPEAT 211 214 23.
FT REPEAT 215 218 24.
FT REPEAT 219 222 25.
FT REPEAT 223 226 26.
FT REPEAT 227 230 27.
FT REPEAT 231 234 28.
FT REPEAT 235 238 29.
FT REPEAT 239 242 30.
FT REPEAT 243 246 31.
FT REPEAT 247 250 32.
FT REPEAT 251 254 33.
FT REPEAT 255 258 34.
FT REPEAT 259 262 35.
FT REPEAT 263 266 36.
FT REPEAT 267 270 37.
FT REPEAT 271 274 38.
FT REPEAT 275 278 39.
FT REPEAT 279 282 40.
FT REPEAT 283 286 41.
FT DOMAIN 337 390 TSP TYPE-1.
SQ SEQUENCE 412 AA; 44420 MW; 1E5EED3DE9065F8 CRC64;

Query Match 48.5%; Score 82; DB 1; Length 412;
Best Local Similarity 78.3%; Pred. No. 0.00036;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 EKXIARMEKASVFNVNNGPSL 24
Db 380 EKXICKMEKCSSVFNVNSSIGL 402

RESULT 4
CSP_PLAFA STANDARD; PRT; 424 AA.
AC P13814;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Circumsporozoite protein precursor (CS).
OS Plasmodium falciparum (isolate t4 / Thailand).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID:5846;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87315205; PubMed=3306373;
RA del Portillo H.A., Nussenzweig R.S., Znea V.;
RT "Circumsporozoite gene of a Plasmodium falciparum strain from
RT Thailand.";
RL Mol. Biochem. Parasitol. 24:289-294(1987).
CC -!- FUNCTION: The circumsporozoite protein is the immunodominant
CC surface antigen on the sporozoite (the infective stage of the
CC malaria parasite that is transmitted from the mosquito to the
CC vertebrate host).
CC -!- MISCELLANEOUS: The C-terminal region is probably used for

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CC anchoring the protein to the cell membrane. The repeat sequences
CC would be the surface antigen of the organism.
CC -!- SIMILARITY: Contains 1 TSP type-1 domain.
CC -----
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CC -----
CC EMBL; M19752; AAA29555.1; -.
CC DR PIR; A54533; A54533.
CC DR InterPro; IPR003067; Crcmsprzoite.
CC DR InterPro; IPR000884; TSP1.
CC DR Pfam; PF00090; TSP1; 1.
CC DR PRINTS; PR01303; CRCMSPRZOITE.
CC DR SMART; SM00209; TSP1; 1.
CC DR PROSITE; PS50092; TSP1; 1.
CC DR Malaria; Sporozoite; Repeat; Signal.
CC FT SIGNAL 1 16
CC FT CHAIN 17 424
CC FT DOMAIN 123 298
CC FT REPEAT 123 126
CC FT REPEAT 127 130
CC FT REPEAT 131 134
CC FT REPEAT 135 138
CC FT REPEAT 139 142
CC FT REPEAT 143 146
CC FT REPEAT 147 150
CC FT REPEAT 151 154
CC FT REPEAT 155 158
CC FT REPEAT 159 162
CC FT REPEAT 163 166
CC FT REPEAT 167 170
CC FT REPEAT 171 174
CC FT REPEAT 175 178
CC FT REPEAT 179 182
CC FT REPEAT 183 186
CC FT REPEAT 187 190
CC FT REPEAT 191 194
CC FT REPEAT 195 198
CC FT REPEAT 199 202
CC FT REPEAT 203 206
CC FT REPEAT 207 210
CC FT REPEAT 211 214
CC FT REPEAT 215 218
CC FT REPEAT 219 222
CC FT REPEAT 223 226
CC FT REPEAT 227 230
CC FT REPEAT 231 234
CC FT REPEAT 235 238
CC FT REPEAT 239 242
CC FT REPEAT 243 246
CC FT REPEAT 247 250
CC FT REPEAT 251 254
CC FT REPEAT 255 258
CC FT REPEAT 259 262
CC FT REPEAT 263 266
CC FT REPEAT 267 270
CC FT REPEAT 271 274
CC FT REPEAT 275 278
CC FT REPEAT 279 282
CC FT REPEAT 283 286
CC FT REPEAT 287 290
CC FT REPEAT 291 294
CC FT REPEAT 295 298
CC FT DOMAIN 349 402
CC SQ SEQUENCE 424 AA; 45610 MW; 710AB14238786CD9 CRC64;
CC Query Match 48.5%; Score 82; DB 1; Length 424;
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Best Local Similarity 78.3%; Pred. No. 0.00037;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2 EKIKAKMEKASSVFNVYVNSGSL 24
Db 392 EKIKCKMEKGVFNVYVNSIGL 414
RESULT 5
CSP_FIAFW STANDARD; PRT; 442 AA.
AC POS307;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Circumsporozoite protein precursor (CS).
OS Plasmodium falciparum (isolate Wellcome).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5848;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87115616; PubMed=3543671;
RA Lockyer M.J.; Schwarz R.T.;
RT "Strain variation in the circumsporozoite protein gene of Plasmodium
RT falciparum.";
RL Mol. Biochem. Parasitol. 22:101-108(1987).
CC -!- FUNCTION: The circumsporozoite protein is the immunodominant
CC surface antigen on the sporozoite (the infective stage of the
CC malaria parasite that is transmitted from the mosquito to the
CC vertebrate host).
CC -!- MISCELLANEOUS: The C-terminal region is probably used for
CC anchoring the protein to the cell membrane. The repeat sequences
CC would be the surface antigen of the organism.
CC -!- SIMILARITY: Contains 1 TSP type-1 domain.
CC -----
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CC -----
CC EMBL; M15505; AAA29554.1; -.
CC DR PIR; A54529; A54529.
CC DR InterPro; IPR003067; Crcmsprzoite.
CC DR InterPro; IPR000884; TSP1.
CC DR Pfam; PF00090; TSP1; 1.
CC DR PRINTS; PR01303; CRCMSPRZOITE.
CC DR SMART; SM00209; TSP1; 1.
CC DR PROSITE; PS50092; TSP1; 1.
CC DR Malaria; Sporozoite; Repeat; Signal.
CC FT SIGNAL 1 16
CC FT CHAIN 17 442
CC FT DOMAIN 134 317
CC FT REPEAT 134 137
CC FT REPEAT 138 141
CC FT REPEAT 142 145
CC FT REPEAT 146 149
CC FT REPEAT 150 153
CC FT REPEAT 154 157
CC FT REPEAT 158 161
CC FT REPEAT 162 165
CC FT REPEAT 166 169
CC FT REPEAT 170 173
CC FT REPEAT 174 177
CC FT REPEAT 178 181
CC FT REPEAT 182 185
CC FT REPEAT 186 189
CC FT REPEAT 190 193
CC FT REPEAT 194 197
CC FT REPEAT 198 201
CC FT REPEAT 201 201
CC CIRCUMSPOROZOITE PROTEIN.
CC 46 X 4 AA TANDEM REPEATS OF N-[AV] - [ND] -
CC P.
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FT REPEAT 202 205 18.
FT REPEAT 206 209 19.
FT REPEAT 210 213 20.
FT REPEAT 214 217 21.
FT REPEAT 218 221 22.
FT REPEAT 222 225 23.
FT REPEAT 226 229 24.
FT REPEAT 230 233 25.
FT REPEAT 234 237 26.
FT REPEAT 238 241 27.
FT REPEAT 242 245 28.
FT REPEAT 246 249 29.
FT REPEAT 250 253 30.
FT REPEAT 254 257 31.
FT REPEAT 258 261 32.
FT REPEAT 262 265 33.
FT REPEAT 266 269 34.
FT REPEAT 270 273 35.
FT REPEAT 274 277 36.
FT REPEAT 278 281 37.
FT REPEAT 282 285 38.
FT REPEAT 286 289 39.
FT REPEAT 290 293 40.
FT REPEAT 294 297 41.
FT REPEAT 298 301 42.
FT REPEAT 302 305 43.
FT REPEAT 306 309 44.
FT REPEAT 310 313 45.
FT REPEAT 314 317 46.
FT DOMAIN 367 420
SQ SEQUENCE 442 AA; 47402 MW; BD57A9A152B85E03 CRC64;

Query Match 48.5%; Score 82; DB 1; Length 442;
Best Local Similarity 78.3%; Pred. No. 0.00038;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 EKXIAKMEKASVFVNVSGL 24
DB 410 EKXICKMEKCSVFVNVSIGL 432

RESULT 6
CON1_RAT STANDARD; PRT; 92 AA.
AC P07490;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Progonadoliberin I precursor [Contains: Gonadoliberin I (LH-RH I)]
DE (luteinizing hormone-releasing hormone I) [Gonadotropin-releasing hormone I] (GNRH I) (Luliberin I); Prolactin release-inhibiting factor I].
GN Rattus norvegicus (Rat).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86094338; PubMed=2867548;
RA Adelman J.P., Mason A.J., Hayflick J.S., Seeburg P.H.;
RT "Isolation of the gene and hypothalamic cDNA for the common precursor of gonadotropin-releasing hormone and prolactin release-inhibiting factor in human and rat.";
RL factor in human and rat.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:179-183(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89384661; PubMed=2476669;
RA Bond C.T., Hayflick J.S., Seeburg P.H., Adelman J.P.;
RT "The rat gonadotropin-releasing hormone: SH locus: structure and hypothalamic expression.";
RL Mol. Endocrinol. 3:1257-1262(1989).
RN [3]

SEQUENCE FROM N.A.
RP TISSUE=Thymus;
RX MEDLINE=93105480; PubMed=1468115;
RA Maier C.C., Marchetti B., Leboeuf R.D., Blalock J.E.;
RT "Thymocytes express a mRNA that is identical to hypothalamic luteinizing hormone-releasing hormone mRNA.";
RL Cell. Mol. Neurobiol. 12:447-454(1992).
RN [4]
RP SEQUENCE OF 1-47 FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=87149087; PubMed=3547652;
RA Adelman J.P., Bond C.T., Douglass J., Herbert E.;
RT "Two mammalian genes transcribed from opposite strands of the same DNA locus";
RL Science 235:1514-1517(1987).
CC -!- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates the secretion of both luteinizing and follicle-stimulating hormones.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Central nervous system.
CC -!- SIMILARITY: Belongs to the GNRH family.
CC -----
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CC -----
DR EMBL; S50870; AAB24572.1; -
DR EMBL; M12579; AAA41263.1; -
DR EMBL; M31670; AAA41264.1; -
DR EMBL; M15527; AAA42141.1; ALT_SEQ.
DR EMBL; M15529; AAA42139.1; -
DR EMBL; M15528; -; NOT_ANNOTATED_CDS.
DR PIR; A40147; RERTG.
DR InterPro; IPR002012; GNRH.
DR InterPro; IPR004079; GonadoliberinI.
DR Pfam; PF00446; GNRH; 1.
DR PRINTS; PR01541; GONADOLIBRNI.
DR PROSITE; PS00473; GNRH; 1.
KW Cleavage on pair of basic residues; Hormone; Amidation; Hypothalamus;
KW Placenta; Signal; Pyrrolidone carboxylic acid.
FT SIGNAL 1 23
FT CHAIN 24 92
FT PEPTIDE 24 33
FT PEPTIDE 37 92
FT ACT_SITE 26 26
FT MOD_RES 24 24
FT MOD_RES 33 33
FT SEQUENCE 92 AA; 10500 MW; 494B5C64DA8A3EB3 CRC64;
Query Match 33.4%; Score 56.5; DB 1; Length 92;
Best Local Similarity 48.3%; Pred. No. 0.35;
Matches 14; Conservative 2; Mismatches 12; Indels 1; Gaps 1;

QY 5 IAKMEKASVFVNVSGLP 32
DB 4 IPKMAAVVLLTVCLGCSQHSYGLRP 32

RESULT 7
CSP_PLABE STANDARD; PRT; 339 AA.
AC P06915;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Circumsporozoite protein precursor (CS).
OS Plasmodium berghei.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

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RT macaques.";
 RL Neuroendocrinology 60:346-359(1994).
 CC -!- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates
 CC the secretion of both luteinizing and follicle-stimulating
 CC hormones.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the GnRH family.
 CC
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 CC
 CC EMBL; M575918; AAB33096.1; --
 DR PIR; I78541; I78541; GnRH.
 DR InterPro; IPR002012; GnRH.
 DR Pfam; PF00446; GnRH; 1.
 DR PRINTS; PR01541; GONADOLIBERNI.
 DR PROSITE; PS00473; GnRH; 1.
 KW Cleavage on pair of basic residues; Hormone; Amidation; Hypothalamus;
 KW Signal; Pyroglutamate carboxylic acid.
 FT NON_TER 1 1
 FT SIGNAL <1 5 BY SIMILARITY.
 FT CHAIN 6 >67 PROGONADOLIBERIN I.
 FT PEPTIDE 6 15 GONADOLIBERIN I.
 FT PEPTIDE 19 >67 GnRH-ASSOCIATED PEPTIDE I.
 FT ACT_SITE 8 8 APPEARS TO BE ESSENTIAL FOR BIOLOGICAL
 FT ACTIVITY (BY SIMILARITY).
 FT MOD_RES 6 6 PYROLIDONE CARBOXYLIC ACID (BY
 FT SIMILARITY)
 FT MOD_RES 15 15 AMIDATION (G-16 PROVIDE AMIDE GROUP) (BY
 FT SIMILARITY).
 FT NON_TER 67 67
 FT SEQUENCE 67 AA; 7573 MW; 505394DAA261A3F2 CRC64;
 Query Match 32.0%; Score 54; DB 1; Length 67;
 Best Local Similarity 90.0%; Pred. No. 0.57; 1; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 23 SLHWSYGLRP 32
 DB 5 SQHWSYGLRP 14
 RESULT 11
 GONI_MOUSE STANDARD; PRT; 90 AA.
 AC P13562;
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Progonadoliberein I precursor [Contains: Gonadoliberein I (LH-RH I)
 DE (Luteinizing hormone-releasing hormone I) (Gonadotropin-releasing
 DE hormone I) (GnRH I) (Luliberin I); Prolactin release-inhibiting factor
 DE I].
 DE GnRH1 OR GnRH.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87069928; PubMed=3024317;
 RA Mason A.J., Hayflick J.S., Zoeller R.T., Young W.S. III,
 RA Phillips H.S., Nikolic K., Seeburg P.H.;
 RT "A deletion truncating the gonadotropin-releasing hormone gene is
 RT responsible for hypogonadism in the hpg mouse."
 RL Science 234:1366-1371(1986).
 CC -!- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates

CC the secretion of both luteinizing and follicle-stimulating
 CC hormones.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the GnRH family.
 CC
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 CC
 CC EMBL; M14872; AAA37717.1; --
 DR PIR; A47578; REMSG.
 DR MGD; MGI:95789; GnRH.
 DR InterPro; IPR002012; GnRH.
 DR Pfam; PF00446; GnRH; 1.
 DR PRINTS; PR01541; GONADOLIBERNI.
 DR PROSITE; PS00473; GnRH; 1.
 KW Cleavage on pair of basic residues; Hormone; Amidation; Hypothalamus;
 KW Placenta; Signal; Pyroglutamate carboxylic acid.
 FT SIGNAL 1 21
 FT CHAIN 22 90 PROGONADOLIBERIN I.
 FT PEPTIDE 22 31 GONADOLIBERIN I.
 FT PEPTIDE 35 90 PROLACTIN RELEASE-INHIBITING FACTOR I.
 FT ACT_SITE 24 24 APPEARS TO BE ESSENTIAL FOR BIOLOGICAL
 FT ACTIVITY
 FT MOD_RES 22 22 PYROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 31 31 AMIDATION (G-32 PROVIDE AMIDE GROUP).
 FT SEQUENCE 90 AA; 10337 MW; 1C0766FA4826E4D9 CRC64;
 Query Match 32.0%; Score 54; DB 1; Length 90;
 Best Local Similarity 90.0%; Pred. No. 0.78; 1; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 23 SLHWSYGLRP 32
 DB 21 SQHWSYGLRP 30
 RESULT 12
 GONI_FIG STANDARD; PRT; 91 AA.
 AC P49921;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Progonadoliberein I precursor [Contains: Gonadoliberein I (LH-RH I)
 DE (Luteinizing hormone-releasing hormone I) (Gonadotropin-releasing
 DE hormone I) (GnRH I) (Luliberin I); GnRH-associated peptide I].
 DE GnRH1 OR GnRH.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Tissue=Hypothalamus;
 RA Weesner G.D., Matteri R.L., Becker B.A.;
 RL Submitted (MAY-1994) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 24-33.
 RX MEDLINE=72114303; PubMed=4946067;
 RA Baba Y., Matsuo H., Schally A.V.;
 RT "Structure of the porcine LH- and FSH-releasing hormone. II.
 RT Confirmation of the proposed structure by conventional sequential
 RT analyses."
 RL Biochem. Biophys. Res. Commun. 44:459-463(1971).
 RN [3]
 RP SYNTHESIS OF GONADOLIBERIN
 RX MEDLINE=72065376; PubMed=4942726;

RA Mateuo H., Arimura A., Nair R.M.G., Schally A.V.;
 RT "Synthesis of the porcine LH- and FSH-releasing hormone by the solid-
 RL phase method."; Biochem. Biophys. Res. Commun. 45:822-827(1971).
 RN [4]
 RP SYNTHESIS OF GONADOLIBERIN.
 RA MEDLINE=72117544; PubMed=4946275;
 RX Baba Y., Arimura A., Schally A.V.;
 RT "On the typtophan residue in porcine LH and FSH-releasing hormone.";
 RL Biochem. Biophys. Res. Commun. 45:483-487(1971).
 CC -!- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates
 CC the secretion of both luteinizing and follicle-stimulating
 CC hormones.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the GnRH family.
 CC
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 CC
 CC EMBL; L32864; AAA31066.1; -.
 DR InterPro; IPR002012; GnRH.
 DR InterPro; IPR004079; Gonadoliberin.
 DR Pfam; PF00446; GnRH; 1.
 DR PRINTS; PR01541; GONADOLIBRN.
 DR PROSITE; PS00473; GnRH; 1.
 KW Cleavage on pair of basic residues; Hormone; Amidation; Hypothalamus;
 KW Placenta; Signal; Pyrrolidone carboxylic acid.
 FT SIGNAL 1 23
 FT CHAIN 24 91 PROGONADOLIBERIN I.
 FT PEPTIDE 24 33 GONADOLIBERIN I.
 FT PEPTIDE 34 91 GnRH-ASSOCIATED PEPTIDE I.
 FT ACT_SITE 26 26 APPEARS TO BE ESSENTIAL FOR BIOLOGICAL
 FT ACTIVITY.
 FT MOD_RES 24 24 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 33 33 AMIDATION (G-34 PROVIDE AMIDE GROUP).
 SQ SEQUENCE 91 AA; 10090 MW; 8340474F32DDAA99 CRC64;
 Query Match 32.0%; Score 54; DB 1; Length 91;
 Best Local Similarity 90.0%; Pred. No. 0.79;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 23 SLHWSYGLRP 32
 Db 23 SCHWSYGLRP 32
 RESULT 13
 GONL_HUMAN STANDARD; PRT; 92 AA.
 AC P01148;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Progonadoliberin I precursor [Contains: Gonadoliberin I (LH-RH I)
 DE (luteinizing hormone-releasing hormone I) (Gonadotropin-releasing
 DE hormone I) (GnRH I) (luliberin I) (Gonadorelin); GnRH-associated
 DE peptide I].
 DE GNRH1 OR GnRH OR LHRH.
 GN Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89366682; PubMed=2671939;
 RA Hayflick J.S., Adelman J.P., Seeburg P.H.;
 RT "The complete nucleotide sequence of the human gonadotropin-releasing
 RT hormone gene.";

RL Nucleic Acids Res. 17:6403-6403(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86094338; PubMed=2867548;
 RA Adelman J.P., Mason A.J., Hayflick J.S., Seeburg P.H.;
 RT "Isolation of the gene and hypothalamic cDNA for the common precursor
 RT of gonadotropin-releasing hormone and prolactin release-inhibiting
 RT factor in human and rat";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:179-183(1986).
 RN [3]
 RP SEQUENCE FROM N.A., AND VARIANT SER-16.
 RX MEDLINE=85012739; PubMed=6090951;
 RA Seeburg P.H., Adelman J.P.;
 RT "Characterization of cDNA for precursor of human luteinizing hormone
 RT releasing hormone.";
 RL Nature 311:666-668(1984).
 RN [4]
 RP SEQUENCE OF 24-33.
 RX MEDLINE=83126573; PubMed=6760865;
 RA Tan L., Rousseau P.;
 RT "The chemical identity of the immunoreactive LHRH-like peptide
 RT biosynthesized in the human placenta.";
 RL Biochem. Biophys. Res. Commun. 109:1061-1071(1982).
 RN [5]
 RP VARIANT SER-16.
 RX MEDLINE=99318093; PubMed=10391209;
 RA Cargill M., Altshuler D., Ireland J., Sklar P., Ardlie K., Patil N.,
 RA Shaw N., Lane C.R., Lim E.P., Kalyanarajan N., Nemesh J., Ziaugra L.,
 RA Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,
 RA Lander E.S.;
 RT "Characterization of single-nucleotide polymorphisms in coding regions
 RT of human genes.";
 RL Nat. Genet. 22:231-238(1999).
 RN [6]
 RP ERRATUM.
 RA Cargill M., Altshuler D., Ireland J., Sklar P., Ardlie K., Patil N.,
 RA Shaw N., Lane C.R., Lim E.P., Kalyanarajan N., Nemesh J., Ziaugra L.,
 RA Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,
 RA Lander E.S.;
 RL Nat. Genet. 23:373-373(1999).
 CC -!- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates
 CC the secretion of both luteinizing and follicle-stimulating
 CC hormones.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- PHARMACOLOGICAL: Available under the names Factrel (Ayerst Labs),
 CC Lutrepulse or Lutrelaf (Ferring Pharmaceuticals) and Relisorm
 CC (Serono).
 CC -!- SIMILARITY: Belongs to the GnRH family.
 CC
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 CC
 CC EMBL; X01059; CAA25526.1; -.
 DR EMBL; M12578; AAA35916.1; -.
 DR EMBL; X15215; CAA33285.1; -.
 DR PIR; S05308; RHUG.
 DR GENE; HGNC:4419; GNRH1.
 DR MIN; 152760; -.
 DR GO; GO:0005625; C:soluble fraction; TAS.
 DR GO; GO:0005183; P:luteinizing hormone-releasing factor activity; TAS.
 DR GO; GO:0007267; P:cell-cell signaling; TAS.
 DR GO; GO:0007275; P:development; TAS.
 DR GO; GO:0008285; P:negative regulation of cell proliferation; TAS.
 DR GO; GO:0007165; P:signal transduction; TAS.
 DR InterPro; IPR002012; GnRH.
 DR InterPro; IPR004079; Gonadoliberin.
 DR Pfam; PF00446; GnRH; 1.
 DR PRINTS; PR01541; GONADOLIBRN.

FT MOD_RES 33 AVIATION (G-34 PROVIDE AMIDE GROUP)
 FT FT (BY SIMILARITY)
 SQ SEQUENCE 95 AA; 10566 MW; 61E79C9930328D73E CRC64;
 Query Match 32.0%; Score 54; DB 1; Length 95;
 Best Local Similarity 52.6%; Pred. No. 0.82;
 Matches 10; Conservative 2; Mismatches 7; Indels 0; Gaps 0;
 QY 14 VFNVNSGPSLHWSYGLRP 32
 DB 14 VMVMSSQGCQHSYGLSP 32
 RESULT 15
 ID GONI_SHEEP STANDARD; PRT; 61 AA.
 AC Q285R8;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Progonadolibrin I precursor [Contains: Gonadolibrin I (LH-RH I)
 DE (Luteinizing hormone-releasing hormone I) (Gonadotropin-releasing
 DE hormone I) (GNRH I) (Luliberin I); GNRH-associated peptide I]
 DE (Fragment).
 DE GNRH1 OR GNRH OR LHRH.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 OC NCBI_TaxID=9940;
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE OF 12-61 FROM N.A.
 RC STRAIN=Western range; TISSUE=Hypothalamus;
 RA Rodriguez R.E., Wise M.E.;
 RL Submitted (OCT-1993) to the EMBL/GenBank/DBJ databases.
 [2]
 RP SEQUENCE OF 1-10.
 RC MEDLINE=72094314; PubMed=4550508;
 RA Burgess R., Butcher M., Amoss M., Ling N., Monahan M., Rivier J.,
 RA Fellows R., Blackwell R., Vale W., Guillemin R.;
 RA "Primary structure of the ovine hypothalamic luteinizing hormone-
 RA releasing factor (LRF) (LH-hypothalamus-LRF-gas chromatography-mass
 RA spectrometry-decapeptide-Edman degradation).";
 RL Proc Natl. Acad. Sci. U.S.A. 69:278-282(1972).
 CC -!- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates
 CC the secretion of both luteinizing and follicle-stimulating
 CC hormones.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the GNRH family.
 CC
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 CC
 CC EMBL: U02517; AAA03433.1; --
 CC InterPro: IPE002012; GnrH.
 CC InterPro: IPR004079; GonadolibrinI.
 CC Pfam: PF00446; GNRH; 1.
 CC PRINTS: PR01541; GNRHOLIBRN1.
 CC PROSITE: PS00473; GNRH; 1.
 CC Cleavage on pair of basic residues; Hormone; Amidation; Hypothalamus;
 CC Placenta; Pyroglutamate carboxylic acid.
 CC
 CC NON TER 1 1
 CC CHAIN 1 >61 PROGNADOLIBRIN I.
 CC PEPTIDE 1 10 GONADOLIBRIN I.
 CC PEPTIDE 14 >61 GNRH-ASSOCIATED PEPTIDE I.
 CC ACT SITE 3 3 APPEARS TO BE ESSENTIAL FOR BIOLOGICAL
 CC ACTIVITY.
 CC
 CC MOD RES 1 1 PYROLIDONE CARBOXYLIC ACID.

FT MOD RES 10 10 AMIDATION (G-11 PROVIDE AMIDE GROUP).
FT NON_TER 61 61
SQ SEQUENCE 61 AA; 6828 MW; 63962A1AE319B8F0 CRC64;
Query Match 30.8%; Score 52; DB 1; Length 61;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 25 HWSYGLRP 32
Db 2 HWSYGLRP 9

Search completed: March 10, 2004, 09:13:55
Job time : 7.03502 secs

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OM protein : protein search, using sw model

Run on: March 10, 2004, 08:58:54 ; Search time 10.8405 Seconds
(without alignments)
133.345 Million cell updates/sec

Title: US-09-848-834A-11

Perfect score: 148

Sequence: 1 QYIKANSKFITIGELPSLHWSYGLRPX 28

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA: *
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2: /cgn2_6/ptodata/2/aaa/5B COMB.pep: *
3: /cgn2_6/ptodata/2/aaa/6A COMB.pep: *
4: /cgn2_6/ptodata/2/aaa/6B COMB.pep: *
5: /cgn2_6/ptodata/2/aaa/PTCUS COMB.pep: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	119.5	80.7	47	1	US-08-446-692-35
2	119.5	80.7	47	2	US-08-488-351A-35
3	112.5	76.0	27	1	US-08-446-692-13
4	112.5	76.0	27	2	US-08-488-351A-13
5	81.5	55.1	31	4	US-09-362-731A-1
6	80	54.1	32	4	US-09-362-731A-5
7	80	54.1	37	1	US-08-446-692-57
8	80	54.1	37	1	US-08-446-692-63
9	80	54.1	37	2	US-08-488-351A-57
10	80	54.1	37	2	US-08-488-351A-63
11	80	54.1	137	4	US-09-362-731A-3
12	78	52.7	50	4	US-08-945-289-8
13	78	52.7	182	4	US-09-396-937-16
14	77	52.0	24	4	US-08-464-496-25
15	77	52.0	24	4	US-08-197-484-110
16	77	52.0	24	5	PCT-US92-07218-25
17	77	52.0	24	5	PCT-US95-02121-110
18	77	52.0	27	4	US-08-464-496-32
19	77	52.0	27	5	PCT-US92-07218-32
20	76	51.4	31	4	US-08-432-483A-2
21	76	51.4	31	4	US-08-945-289-2
22	74	50.0	15	2	US-08-319-704-10
23	74	50.0	15	2	US-08-661-052-6
24	74	50.0	15	2	US-08-460-502-7
25	74	50.0	15	3	US-09-046-373-2
26	74	50.0	15	3	US-09-188-082-6
27	74	50.0	15	4	US-09-364-088-6

Sequence 6, Appli
Sequence 7, Appli
Sequence 4, Appli
Sequence 13, Appli
Sequence 34, Appli
Sequence 1, Appli
Sequence 69, Appli
Sequence 55, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 40, Appli
Sequence 23, Appli
Sequence 23, Appli
Sequence 7, Appli
Sequence 63, Appli
Sequence 18, Appli
Sequence 17, Appli
Sequence 16, Appli

28 74 50.0 15 4 US-09-102-716-6
29 74 50.0 15 4 US-09-148-711A-7
30 74 50.0 15 4 US-08-716-249-4
31 74 50.0 15 4 US-09-362-731A-13
32 74 50.0 15 4 US-09-396-937-34
33 74 50.0 15 4 US-09-405-988A-1
34 74 50.0 15 5 PCT-US93-11703-69
35 74 50.0 16 3 US-09-248-588-55
36 74 50.0 17 1 US-08-446-692-4
37 74 50.0 17 3 US-08-488-351A-4
38 74 50.0 17 3 US-09-100-409A-40
39 74 50.0 17 4 US-08-472-701-23
40 74 50.0 17 5 PCT-US95-08596-23
41 74 50.0 17 5 PCT-US95-13841-7
42 74 50.0 31 5 PCT-US93-11703-63
43 74 50.0 173 4 US-09-396-937-18
44 74 50.0 853 4 US-08-913-880C-17
45 74 50.0 858 4 US-08-913-880C-16

ALIGNMENTS

RESULT 1
US-08-446-692-35
; Sequence 35 Application US/08446692
; Patent No. 5759551
; GENERAL INFORMATION:
; APPLICANT: Ladd, Anna
; APPLICANT: Wang, Chang Yi
; APPLICANT: Zamb, Timothy
; TITLE OF INVENTION: Immunogenic LHRH peptide constructs
; TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maria C.H. Lin
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10154-0053
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,692
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria C.H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4146 US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)415-8745
; TELEFAX: (516)751-6849
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 47 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-446-692-35

Query Match 80.7%; Score 119.5; DB 1; Length 47;
Best Local Similarity 88.9%; Pred. No. 8e-12;
Matches 24; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 QYIKANSKFITIGELPSLHWSYGLRP 27

DB 21 QYIKANSKFITIGELGGE-HWSYGLRP 46

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; TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
;
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maria C.H. Lin
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10154-0053
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,692
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria C.H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4146 US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)415-8745
; TELEFAX: (516)751-6849
;
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
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; US-08-446-692-13
;
; Query Match 76.0%; Score 112.5; DB 1; Length 27;
; Best Local Similarity 85.2%; Pred. No. 5.4e-11;
; Matches 23; Conservative 0; Mismatches 1; Indels 3; Gaps 1;
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; QY 1 QYKANSKFIGITELGPSLHWSYGLRP 27
; DB 3 QYKANSKFIGITELTE--HWSYGLRP 26
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; RESULT 4
; US-08-488-351A-13
; Sequence 13, Application US/08488351A
; Patent No. 5843446
;
; GENERAL INFORMATION:
; APPLICANT: Ladd, Anna
; APPLICANT: Wang, Chang Yi
; APPLICANT: Zamb, Timothy
;
; TITLE OF INVENTION: Immunogenic LHRH peptide constructs
;
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maria C.H. Lin
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10154-0053
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,351A
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/446,692
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/229,275
; FILING DATE: 14-APR-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/057,166
; FILING DATE: 27-APR-1992
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria C.H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4146 US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)415-8745
; TELEFAX: (516)751-6849
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-488-351A-13

Query Match 76.0%; Score 112.5; DB 2; Length 27;
Best Local Similarity 85.2%; Pred. No. 5.4e-11;
Matches 23; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

QY 1 QYIKANSKFIGITELGPSLHWSYGLRP 27
Db 3 QYIKANSKFIGITELE---HWSYGLRP 26

RESULT 5
US-09-362-731A-1
; Sequence 1, Application US/09362731A
; Patent No. 6602509
; GENERAL INFORMATION:
; APPLICANT: SAINT-REMY, Jean-Marie
; APPLICANT: JACQUEMIN, Marc
; TITLE OF INVENTION: COMPOUND AND METHOD FOR THE PREVENTION AND/OR THE TREATMENT OF AL
; FILE REFERENCE: 99-0720*/LC/01699
; CURRENT APPLICATION NUMBER: US/09/362,731A
; CURRENT FILING DATE: 1999-07-29
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin Version 2.1
; SEQ ID NO 1
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide
; US-09-362-731A-1

Query Match 55.1%; Score 81.5; DB 4; Length 31;
Best Local Similarity 61.3%; Pred. No. 4.9e-06;
Matches 19; Conservative 0; Mismatches 3; Indels 9; Gaps 1;

QY 1 QYIKANSKFIGITELG-----PSLHWS 22
Db 1 QYIKANSKFIGITELGGHKEIKVLVPGCHGS 31

RESULT 6
US-09-362-731A-5
; Sequence 5, Application US/09362731A
; Patent No. 6602509
; GENERAL INFORMATION:
; APPLICANT: SAINT-REMY, Jean-Marie
; APPLICANT: JACQUEMIN, Marc
; TITLE OF INVENTION: COMPOUND AND METHOD FOR THE PREVENTION AND/OR THE TREATMENT OF AL
; FILE REFERENCE: 99-0720*/LC/01699
; CURRENT APPLICATION NUMBER: US/09/362,731A
; CURRENT FILING DATE: 1999-07-29

; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin Version 2.1
; SEQ ID NO 5
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide
; US-09-362-731A-5

Query Match 54.1%; Score 80; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 8.7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYIKANSKFIGITELG 16
Db 1 QYIKANSKFIGITELG 16

RESULT 7
US-08-446-692-57
; Sequence 57, Application US/08446692
; Patent No. 5759551
; GENERAL INFORMATION:
; APPLICANT: Ladd, Anna
; APPLICANT: Wang, Chang Yi
; APPLICANT: Zamb, Timothy
; TITLE OF INVENTION: Immunogenic LHRH peptide constructs
; TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maria C.H. Lin
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,692
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria C.H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4146 US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)415-8745
; TELEFAX: (516)751-6849
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-446-692-57

Query Match 54.1%; Score 80; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYIKANSKFIGITELG 16
Db 21 QYIKANSKFIGITELG 36

RESULT 8
US-08-446-692-63
; Sequence 63, Application US/08446692
```

```

; Patent No. 5759551
; GENERAL INFORMATION:
; APPLICANT: Ladd, Anna
; APPLICANT: Wang, Chang Yi
; APPLICANT: Zamb, Timothy
; TITLE OF INVENTION: Immunogenic LHRH peptide constructs
; TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maria C.H. Lin
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,692
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria C.H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4146 US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)415-8745
; TELEFAX: (516)751-6849
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; US-08-446-692-63

Query Match 54.1%; Score 80; DB 1; Length 37;
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYIKANSKFIGITELG 16
Db 5 QYIKANSKFIGITELG 20

RESULT 9
US-08-488-351A-57
; Sequence 57 Application US/08488351A
; Patent No. 5843446
; GENERAL INFORMATION:
; APPLICANT: Ladd, Anna
; APPLICANT: Wang, Chang Yi
; APPLICANT: Zamb, Timothy
; TITLE OF INVENTION: Immunogenic LHRH peptide constructs
; TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maria C.H. Lin
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,351A

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; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/446,692
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/229,275
; FILING DATE: 14-APR-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/057,166
; FILING DATE: 27-APR-1992
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria C.H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4146 US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)415-8745
; TELEFAX: (516)751-6849
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-488-351A-57

Query Match 54.1%; Score 80; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYIKANSKFIGITELG 16
Db 21 QYIKANSKFIGITELG 36

RESULT 10
US-08-488-351A-63
; Sequence 63 Application US/08488351A
; Patent No. 5843446
; GENERAL INFORMATION:
; APPLICANT: Ladd, Anna
; APPLICANT: Wang, Chang Yi
; APPLICANT: Zamb, Timothy
; TITLE OF INVENTION: Immunogenic LHRH peptide constructs
; TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maria C.H. Lin
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,351A
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/446,692
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/229,275
; FILING DATE: 14-APR-1994
; CLASSIFICATION: 424

```

```

;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/057,166
; FILING DATE: 27-APR-1992
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria C.H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4146 US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 415-8745
; TELEFAX: (516) 751-6849
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-488-351A-63

Query Match 54.1%; Score 80; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYKANSKFIFGITELG 16
Db 5 QYKANSKFIFGITELG 20

RESULT 11
US-09-362-731A-3
; Sequence 3, Application US/09362731A
; Patent No. 6602509
; GENERAL INFORMATION:
; APPLICANT: SAINT-REMY, Jean-Marie
; APPLICANT: JACQUEMIN, Marc
; TITLE OF INVENTION: COMPOUND AND METHOD FOR THE PREVENTION AND/OR THE TREATMENT OF AL
; FILE REFERENCE: 99-0720*/LC/01699
; CURRENT APPLICATION NUMBER: US/09/362,731A
; CURRENT FILING DATE: 1999-07-29
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 3
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide
; US-09-362-731A-3

Query Match 54.1%; Score 80; DB 4; Length 137;
Best Local Similarity 100.0%; Pred. No. 4.5e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYKANSKFIFGITELG 16
Db 2 QYKANSKFIFGITELG 17

RESULT 12
US-08-945-289-8
; Sequence 8, Application US/08945289
; Patent No. 6555113
; GENERAL INFORMATION:
; APPLICANT: Rittershaus, Charles, W.
; APPLICANT: Thomas, Lawrence J.
; TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER
; TITLE OF INVENTION: TRANSFER PROTEIN (CETP) ACTIVITY
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yankwich & Associates
; STREET: 130 Bishop Allen Drive
; CITY: Cambridge
; STATE: Massachusetts

;
; COUNTRY: USA
; ZIP: 02139
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/945,289
; FILING DATE: October 17, 1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/432,483
; FILING DATE: May 1, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Leon R. Yankwich
; REGISTRATION NUMBER: 30,237
; REFERENCE/DOCKET NUMBER: TCS-411.1P US
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL:
; ANTI-SENSE:
; FEATURE:
; NAME/KEY:
; LOCATION:
; US-08-945-289-8

Query Match 52.7%; Score 78; DB 4; Length 50;
Best Local Similarity 94.1%; Pred. No. 3e-05;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QYKANSKFIFGITELGP 17
Db 2 QYKANSKFIFGITELFP 18

RESULT 13
US-09-396-937-16
; Sequence 16, Application US/09396937
; Patent No. 6645500
; GENERAL INFORMATION:
; APPLICANT: M&E Biotech A/S
; APPLICANT: HALKIER, Torben
; APPLICANT: HANING, Jesper
; TITLE OF INVENTION: Method for Down-Regulating Osteoprotegerin Ligand
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 22021 PC 1
; CURRENT APPLICATION NUMBER: US/09/396,937
; CURRENT FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 182
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: between murine OPGL residues 158-316 with tetanus
; OTHER INFORMATION: toxoid P2 epitope introduced, and His tag
; US-09-396-937-16

Query Match 52.7%; Score 78; DB 4; Length 182;
Best Local Similarity 77.3%; Pred. No. 0.00013;
Matches 17; Conservative 1; Mismatches 0; Indels 4; Gaps 1;

QY 1 QYKANSKFIFGITELGPSLHWS 22
Db 113 QYKANSKFIFGITELGPSLHWS 130
```

```

RESULT 14
US-08-464-496-25
; Sequence 25, Application US/08464496
; Patent No. 632789
; GENERAL INFORMATION:
; APPLICANT: Epimmune, Inc.
; APPLICANT: Vitello, Maria
; APPLICANT: Chestnut, Robert
; TITLE OF INVENTION: HLA-RESTRICTED HEPATITIS B VIRUS CTL
; TITLE OF INVENTION: EPITOPE
; FILE REFERENCE: 39963-20001.13
; CURRENT APPLICATION NUMBER: US/08/464,496
; CURRENT FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: 07/935,811
; PRIOR FILING DATE: 1992-08-26
; PRIOR APPLICATION NUMBER: 07/874,491
; PRIOR FILING DATE: 1992-04-27
; PRIOR APPLICATION NUMBER: 07/827,682
; PRIOR FILING DATE: 1992-01-29
; PRIOR APPLICATION NUMBER: 07/749,568
; PRIOR FILING DATE: 1991-08-26
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Oligopeptide
US-08-464-496-25

Query Match 52.0%; Score 77; DB 4; Length 24;
Best Local Similarity 88.9%; Pred. No. 1.9e-05;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QYKANSKFGITELGPS 18
Db 1 QYKANSKFGITELGPS 18

RESULT 15
US-08-197-484-110
; Sequence 110, Application US/08197484
; Patent No. 8419931
; GENERAL INFORMATION:
; APPLICANT: VITIELLO, Maria A.
; APPLICANT: CHESTNUT, Robert W.
; APPLICANT: SETTE, Alessandro D.
; APPLICANT: CELIS, Esteban
; APPLICANT: GRAY, Howard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; TITLE OF INVENTION: CTL IMMUNITY
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/197,484
; FILING DATE: 16-FEB-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/935,811
; FILING DATE: 26-AUG-1992

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; PRIOR APPLICATION DATA: US 07/874,491
; FILING DATE: 27-APR-1992
; PRIOR APPLICATION DATA: US 07/827,682
; FILING DATE: 29-JAN-1992
; PRIOR APPLICATION DATA: US 07/749,568
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-26-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (206) 623-6793
; INFORMATION FOR SEQ ID NO: 110:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-197-484-110

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```

Query Match 52.0%; Score 77; DB 4; Length 24;
Best Local Similarity 88.9%; Pred. No. 1.9e-05;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 QYKANSKFGITELGPS 18
Db 1 QYKANSKFGITELGPS 18

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Search completed: March 10, 2004, 09:28:54
Job time : 10.8405 secs

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OM protein - protein search, using sw model
Run on: March 10, 2004, 08:58:54 ; Search time 10.2724 Seconds
(without alignments)
309.015 Million cell updates/sec

Title: US-09-848-834A-12
Perfect score: 169
Sequence: 1 DEKIAKMKKASSVFNVNGPSLWVGLRPX 33

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78: *
1: Pirl: *
2: Pirl: *
3: Pirl: *
4: Pirl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	82	48.5	388	2 A39756	circumsporozoite p
2	82	48.5	405	2 S05428	circumsporozoite p
3	82	48.5	412	1 OZQAF	circumsporozoite p
4	82	48.5	424	2 A54533	circumsporozoite p
5	82	48.5	442	2 A54529	circumsporozoite p
6	56.5	33.4	92	1 RHRTG	gonadoliberin prec
7	55	32.5	264	2 A44969	circumsporozoite p
8	55	32.5	332	1 OZQMB	circumsporozoite p
9	55	32.5	348	1 OZQMB	circumsporozoite p
10	55	32.5	360	2 AD2528	circumsporozoite p
11	55	32.5	367	1 OZQMY	integrate-recombin
12	54	32.0	67	2 I78541	gonadoliberin prec
13	54	32.0	90	1 RHMSG	gonadoliberin prec
14	54	32.0	92	1 RHMSG	gonadoliberin - pi
15	52	30.8	10	1 RHPGG	gonadoliberin - sh
16	52	30.8	10	1 RHSGG	gonadoliberin - sh
17	52	30.8	89	2 IS423	gonadoliberin prote
18	52	30.8	994	2 S00960	hypothetical prote
19	51	30.2	91	2 JC7393	medaka-type gonado
20	51	30.2	429	2 A54504	circumsporozoite p
21	51	30.2	485	2 A60610	circumsporozoite p
22	51	30.2	507	2 H82378	probable long-chain
23	50	29.6	1484	2 C97196	probable membrane
24	50	29.6	2339	2 A45597	DNA-directed RNA p
25	49.5	29.3	630	2 A53359	VSG expression sit
26	49.5	29.3	630	2 S13724	ESAG 8 protein - T
27	49.5	29.3	999	2 S15961	hypothetical protei
28	49.5	29.3	1265	2 S57968	ran-binding protei
29	49.5	29.3	3176	2 CGH3A	collagen alpha 3(V

30	49	29.0	532	2 S27373	beta-fructofuranos
31	49	29.0	1146	2 S40311	integrin - fruit f
32	48.5	28.7	630	1 BWUT8Q	regulatory protein
33	48	28.4	10	1 RHAQ1	gonadoliberin I -
34	48	28.4	66	2 T43096	hypothetical prote
35	48	28.4	92	2 I50644	gonadoliberin I pr
36	48	28.4	260	2 T41554	hypothetical prote
37	48	28.4	525	2 T40088	RHOGEF domain cont
38	48	28.4	3133	2 S52093	hemocytin - silkwo
39	47.5	28.1	98	2 I50739	gonadotropin-relea
40	47.5	28.1	562	2 JQ1036	63k aducin-like p
41	47.5	28.1	664	2 AB1430	hypothetical prote
42	47.5	28.1	664	2 AH1803	hypothetical prote
43	47.5	28.1	668	1 UYPVME	noncapsid protein
44	47.5	28.1	2244	2 F90563	hypothetical prote
45	47	27.8	217	2 A98196	hypothetical prote

ALIGNMENTS

RESULT 1
A39756
Circumsporozoite protein - Plasmodium reichenowi
C:Species: Plasmodium reichenowi
C>Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 20-Aug-1999
C:Accession: A39756
R:Lal, A.A.; Goldman, I.F.
J. Biol. Chem. 266, 6686-6689, 1991
A:Title: Circumsporozoite protein gene from Plasmodium reichenowi, a chimpanzee malar
A:Reference number: A39756; MUID:91201303; PMID:2016283
A:Accession: A39756
A>Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-388 <LAL>
A:Cross-references: GB:M60972; NID:G160228; PIDN:AAA29561.1; PID:G160229
C:Superfamily: Circumsporozoite protein; thrombospondin type 1 repeat homology
F:312-366/Domain: thrombospondin type 1 repeat homology <THR1>

Query Match 48.5%; Score 82; DB 2; Length 388;
Best Local Similarity 78.3%; Pred. NO. 0.00083;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 EKIKMKKASSVFNVNGPSL 24
Db 356 EKIKMKKASSVFNVNGPSL 378
RESULT 2
S05428
Circumsporozoite protein - malaria parasite (Plasmodium falciparum) (isolate NF54)
C:Species: Plasmodium falciparum
C>Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jun-2000
C:Accession: S05428; A45527; I60857
R:Campbell, J.R.
Nucleic Acids Res. 17, 5854, 1989
A:Title: DNA sequence of the gene encoding a Plasmodium falciparum malaria candidate v
A:Reference number: S05428; MUID:89345189; PMID:2668895
A:Accession: S05428
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-405 <CAM>
A:Cross-references: EMBL:X15363
R:Caspers, P.; Gentz, R.; Matile, H.; Pink, J.R.; Sinigaglia, F.
Mol. Biochem. Parasitol. 35, 185-190, 1989
A:Title: The circumsporozoite protein gene from NF54, a Plasmodium falciparum isolate
A:Reference number: A45527; MUID:89364998; PMID:2671723
A:Accession: A45527
A>Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-405 <CAS>
A:Cross-references: GB:M22982; GB:J04650; NID:G160168; PIDN:AAA29527.1; PID:G160169
R:Lockyer, M.J.; Marsh, K.; Newbold, C.I.

RESULT 3

Query Match	48.5%	Score 82	DB 1	Length 412
Best Local Similarity	78.3%	Pred. No. 0.00089		
Matches 18	Conservative	0	Mismatches 5	Indels 0
			Gaps 0	

Query Match	48.5%;	Score 82;	DB 2;	Length 424;
Best Local Similarity	78.3%;	Pred. No. 0.00092;		
Matches 18;	Conservative	0;	Mismatches 5;	Indels 0;
			Gaps	0;

C;Superfamily: gonadoliberin
C;Keywords: amidated carboxyl end; hormone; hypothalamus; placenta; pyroglutamic acid;
F;1-23/Domain: signal sequence #status predicted <SIG>

F:24-92/Product: progonaoliberin #status predicted <PCN>
 F:24-33/Product: gonadolibirin #status predicted <Gln>
 F:37-92/Product: prolactin release-inhibiting factor #status predicted <PIF>
 F:24/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
 F:33/Modified site: amidated carboxyl end (Gly) (amide in mature form from following gly

Query Match 33.4%; Score 56.5; DB 1; Length 92;
 Best Local Similarity 48.3%; Pred. No. 0.72;
 Matches 14; Conservative 2; Mismatches 12; Indels 1; Gaps 1;

QY 5 IAKVEKASSVFNVNSG-PSLHWSYGLRP 32
 DB 4 IPKLVAAVLLTVLCGSSQHSYGLRP 32

RESULT 7
 A44969
 Circumsporozoite protein precursor - Plasmodium yoelii nigeriensis
 C:Species: Plasmodium yoelii nigeriensis
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 01-Dec-1995
 C:Accession: A44969
 R:Colomer-Gould, V.; Enea, V.
 Mol. Biochem. Parasitol. 43, 51-58, 1990
 A:Title: Plasmodium yoelii nigeriensis circumsporozoite gene structure and its implicati
 A:Reference number: A44969; MUID:91148645; PMID:2290446
 A:Accession: A44969
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-264 <COL>
 A:Cross-references: GB:M32350
 C:Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology
 F:190-242/Domain: thrombospondin type 1 repeat homology <THR1>

Query Match 32.5%; Score 55; DB 2; Length 264;
 Best Local Similarity 47.4%; Pred. No. 3.9;
 Matches 9; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 2 EKKIAMEKASSVFNVNS 20
 DB 232 DTEICKMDKCSIFNIVSN 250

RESULT 8
 OZZQMB
 Circumsporozoite protein precursor - Plasmodium berghei (strain NK65)
 N:Alternate names: sporozoite surface antigen
 C:Species: Plasmodium berghei
 C:Date: 30-Sep-1987 #sequence_revision 28-Jul-1995 #text_change 16-Jul-1999
 C:Accession: A44948; A25083; S13446
 R:Janat, D.E.
 Mol. Biochem. Parasitol. 39, 151-154, 1990
 A:Title: Sequence of the circumsporozoite gene of Plasmodium berghei ANKA clone and NK65
 A:Reference number: A44948; MUID:90158693; PMID:2406593
 A:Accession: A44948
 A:Molecule type: DNA
 A:Residues: 1-332 <LAN>
 A:Cross-references: GB:M28887
 R:Schinger, D.J.; Arnott, D.E.; Tam, J.P.; Nussenzweig, V.; Enea, V.
 Mol. Cell. Biol. 6, 3965-3972, 1986
 A:Title: Circumsporozoite protein of Plasmodium berghei: gene cloning and identification
 A:Reference number: A25083; MUID:87089740; PMID:2432395
 A:Accession: A25083
 A:Molecule type: DNA
 A:Residues: 1-26, 'I', 28-68, 'PMRR', 75-126, 'P', 128-134, 'PPNANDP', 135-332 <EIC>
 A:Cross-references: GB:M4135; NID:gl60245; PIDN:AAA29577.1; PID:gl60246
 R:Webster, J.L.; Egan, J.B.; Lyon, J.A.; Wirtz, R.A.; Charoenvit, Y.; Maloy, W.L.; Hockmeyer, J.
 Exp. Parasitol. 63, 295-300, 1987
 A:Title: Plasmodium berghei: cloning of the circumsporozoite protein gene.
 A:Reference number: S13446; MUID:87218962; PMID:3556207
 A:Accession: S13446
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 61-122, 'A', 124-332 <WEB>

A:Cross-references: GB:M25445; NID:9160177; PIDN:AAA29531.1; PID:gl60178
 C:Comment: there are three distinct regions in the mature circumsporozoite protein, th
 obic membrane-anchoring sequence.
 C:Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology
 C:Keywords: sporozoite; surface antigen; tandem repeat
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-332/Product: circumsporozoite protein #status predicted <MAT>
 F:94-189/Region: 8-residue repeats
 F:199-230/Region: 2-residue repeats
 F:258-310/Domain: thrombospondin type 1 repeat homology <THR1>

Query Match 32.5%; Score 55; DB 1; Length 332;
 Best Local Similarity 47.4%; Pred. No. 5;
 Matches 9; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 2 EKKIAMEKASSVFNVNS 20

DB 300 DTEICKMDKCSIFNIVSN 318

RESULT 9
 OZZQMB

Circumsporozoite protein precursor - Plasmodium berghei (strain ANKA clone 2.341)
 N:Alternate names: sporozoite surface antigen
 C:Species: Plasmodium berghei
 C:Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 16-Jul-1999
 C:Accession: S07873; S12571
 R:Lockyer, M.J.; Davies, C.S.; Suhrbier, A.; Sinden, R.E.

Nucleic Acids Res. 18, 376, 1990
 A:Title: Nucleotide sequence of the Plasmodium berghei circumsporozoite protein gene f
 A:Reference number: S07873; MUID:90221834; PMID:2183186
 A:Accession: S07873
 A:Molecule type: DNA
 A:Residues: 1-348 <LOC>

A:Cross-references: EMBL:X17606
 R:Lockyer, M.J.
 Submitted to the EMBL Data Library, November 1989
 A:Reference number: S12571
 A:Accession: S12571
 A:Molecule type: DNA

A:Residues: 1-59, 'I', 61-81, 83-348 <LOC2>
 A:Cross-references: EMBL:X17606; NID:g9784; PIDN:CAA35608.1; PID:g9785

C:Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology

C:Keywords: tandem repeat

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-348/Product: circumsporozoite protein #status predicted <MAT>

F:94-205/Region: 8-residue repeats

F:215-247/Region: 2-residue repeats

F:274-326/Domain: thrombospondin type 1 repeat homology <THR1>

Query Match 32.5%; Score 55; DB 1; Length 348;
 Best Local Similarity 47.4%; Pred. No. 5.3;
 Matches 9; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 2 EKKIAMEKASSVFNVNS 20

DB 316 DTEICKMDKCSIFNIVSN 334

RESULT 10
 AD2528

Integrase-recombinase protein [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC712
 C:Species: Nostoc sp. PCC 7120

A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002

C:Accession: AD2528

R:Kanehiko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriq

NA Res. 8, 205-213, 2001

A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A

A:Reference number: AB1807; MUID:21595285; PMID:11759840

A:Accession: AD2528

A>Status: preliminary

QY 23 SLHWSYGRLP 32
| | | | |
Db 5 SQHWSGLRP 14

RESULT 13
RHMSG
gonadoliberin precursor - mouse
N;Alternate names: gonadotropin-releasing hormone (GnRH); luteinizing hormone releasing
N;Contains: gonadoliberin; gonadoliberin-associated protein (GAP)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1993 #sequence_revision 18-Mar-1997 #text_change 18-Jun-1999
C;Accession: A47578
R;Mason, A.J.; Hayflick, J.S.; Zoeller, R.T.; Young III, W.S.; Phillips, H.S.; Nikolics
Science 234, 1366-1371, 1986
A;Title: A deletion truncating the gonadotropin-releasing hormone gene is responsible f
A;Reference number: A47578; MUID:87069928; PMID:3024317
A;Accession: A47578
A:Molecule type: DNA
A;Residues: 1-90 <MAS>
A;Cross-references: EMBL:M14872; NID:g193576; PIDN:AAA37717.1; PID:g387175
C;Genetics:
A;Introns: 45/3; 77/3
C;Function:
A;Description: gonadoliberin stimulates pituitary secretion of lutropin and follitropin
A;Note: gonadoliberin-associated protein may have prolactin release inhibiting activity
C;Superfamily: gonadoliberin
C;Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid
F;1-23/Domain: signal sequence #status predicted <SIG>
F;22-31/Product: gonadoliberin #status predicted <GLB>
F;35-90/Product: gonadoliberin-associated protein #status predicted <GAP>
F;22/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicte
F;31/Modified site: amidated carboxyl end (Gly) (amide in mature form from following gl

Query Match 32.08; Score 54; DB 1; Length 90;
Best Local Similarity 90.08; Pred. No. 1.6; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 1;

QY 23 SLHWSYGRLP 32
| | | | |
Db 21 SQHWSGLRP 30

RESULT 14
RHJUG
gonadoliberin precursor [validated] - human
N;Alternate names: gonadotropin releasing hormone (GnRH); luteinizing hormone releasing
N;Contains: gonadoliberin-associated protein (GAP); progonadoliberin
C;Species: Homo sapiens (man)
C;Date: 17-Mar-1987 #sequence_revision 21-Jul-1995 #text_change 08-Dec-2000
C;Accession: S05308; A26173; X33342; A90108; A01410; S45718
R;Hayflick, J.S.; Adelman, J.P.; Seeburg, P.H.
Nucleic Acids Res. 17, 6403-6404, 1989
A;Title: The complete nucleotide sequence of the human gonadotropin-releasing hormone s
A;Reference number: S05308; MUID:89366682; PMID:2671939
A;Accession: S05308
A;Status: translation not shown
A:Molecule type: DNA
A;Residues: 1-92 <HAY>
A;Cross-references: EMBL:X15215; NID:g31955; PIDN:CAA33285.1; PID:g31956
R;Adelman, J.P.; Mason, A.J.; Hayflick, J.S.; Seeburg, P.H.
Proc. Natl. Acad. Sci. U.S.A. 83, 179-183, 1986
A;Title: Isolation of the gene and hypothalamic cDNA for the common precursor of gonado
A;Reference number: A94090; MUID:86094338; PMID:2867548
A;Accession: A26173
A:Molecule type: mRNA
A;Residues: 1-92 <ADS>
A;Cross-references: GB:M12578; NID:g183418; PIDN:AAA35916.1; PID:g386749
R;Seeburg, P.H.; Adelman, J.P.
Nature 311, 666-668, 1984
A;Title: Characterization of cDNA for precursor of human luteinizing hormone releasing

A:Reference number: A93342; MUID:85012739; PMID:6090951
 A:Accession: A93342
 A:Molecule type: mRNA
 A:Residues: 1-15, 'S', 17-92 <SEE>
 A:Cross-references: GB:X01059; NID:G34356; PIDN:CAA25526.1; PID:G34357
 A:Experimental source: placenta
 R:Tan, L.; Rouseau, P.
 Biochem. Biophys. Res. Commun. 109, 1061-1071, 1982
 A:Title: The chemical identity of the immunoreactive LHRH-like peptide biosynthesized in
 A:Reference number: A90108; MUID:83126573; PMID:6760865
 A:Accession: A90108
 A:Molecule type: protein
 A:Residues: 24-33 <TAN>
 A:Experimental source: placental trophoblasts
 R:Leibovitz, D.; Koch, Y.; Pitzer, F.; Fridkin, M.; Dantes, A.; Baumeister, W.; Amsterda
 FEBS Lett. 346, 203-206, 1994
 A:Title: Sequential degradation of the neuropeptide gonadotropin-releasing hormone by th
 A:Reference number: S45718; MUID:94283597; PMID:8013634
 A:Contents: annotation; degradation pathway of synthetic hormone
 C:Genetics:
 A:Gene: GDB:GNRH; LHRH; GRH
 A:Cross-references: GDB:133746; OMIM:227200; OMIM:152760
 A:Map position: 8p21-8p11.2
 A:Introns: 47/3; 75/3
 C:Function:
 A:Description: gonadoliberein stimulates pituitary secretion of lutropin and follitropin
 A:Note: gonadoliberein-associated protein may have prolactin release inhibiting activity
 C:Superfamily: gonadoliberein
 C:Keywords: amidated carboxyl end; hormone; hypothalamus; placenta; pyroglutamic acid
 F:1-23/Domain: signal sequence #status Predicted <SIG>
 F:24-32/Product: progadoliberein #status Predicted <PGN>
 F:37-92/Product: gonadoliberein #status experimental <MAR>
 F:24/Modified site: pyroglutamic acid (Gln) (in mature form) #status experimen
 F:33/Modified site: amidated carboxyl end (Gly) (amide in mature form from following gly

Query Match 32.0%; Score 54; DB 1; Length 92;
 Best Local Similarity 90.0%; Pred No. 1.6;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 23 SLHWSYGLRP 32
 | | | | |
 DB 23 SQHWSYGLRP 32

RESULT 15
 RHPGG
 Gonadoliberein - pig
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 18-Mar-1997
 C:Accession: A01411
 R:Baba, Y.; Matsuo, H.; Schally, A.V.
 Biochem. Biophys. Res. Commun. 44, 459-463, 1971
 A:Title: Structure of the porcine LH- and FSH-releasing hormone. II. Confirmation of the
 A:Reference number: A90172; MUID:72114303; PMID:4946067
 A:Accession: A01411
 A:Molecule type: protein
 A:Residues: 1-10 <BAB>
 R:Matsuo, H.; Arimura, A.; Nair, R.M.G.; Schally, A.V.
 Biochem. Biophys. Res. Commun. 45, 822-827, 1971
 A:Title: Synthesis of the porcine LH- and FSH-releasing hormone by the solid-phase metho
 A:Reference number: A90176; MUID:72065376; PMID:4942726
 A:Contents: annotation; synthesis
 A:Note: the synthetic and natural hormones have the same physicochemical and biological
 R:Baba, Y.; Arimura, A.; Schally, A.V.
 Biochem. Biophys. Res. Commun. 45, 483-487, 1971
 A:Title: On the tryptophan residue in porcine LH and FSH-releasing hormone.
 A:Reference number: A90175; MUID:72117544; PMID:4946275
 A:Contents: annotation
 A:Note: Trp-3 appears to be essential for biological activity
 C:Comment: This hypothalamic hormone stimulates the secretion of both luteinizing and fo
 C:Superfamily: gonadoliberein
 C:Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F:10/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 30.8%; Score 52; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.26;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 HWSYGLRP 32
 | | | | |
 DB 2 HWSYGLRP 9

Search completed: March 10, 2004, 09:16:48
 Job time : 11.3312 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 10, 2004, 09:16:59 ; Search time 22.0078 Seconds
(without alignments)
268.645 Million cell updates/sec

Title: US-09-848-834A-11
Perfect score: 148
Sequence: 1 QYIKANSKFIGITELGSLHWSYGLRPX 28

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 809742 seqs, 211153259 residues

Total number of hits satisfying chosen parameters: 809742

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
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15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	147	99.3	28	9	US-09-848-834A-11
2	136	91.9	46	9	US-09-848-834A-19
3	112.5	76.0	27	14	US-10-076-674-7
4	112.5	76.0	27	15	US-10-355-161A-7
5	82	55.4	158	14	US-10-297-942-16
6	81.5	55.1	31	14	US-10-237-656-1
7	81.5	55.1	33	9	US-09-848-834A-12
8	81	54.7	194	14	US-10-295-074-47
9	80	54.1	32	14	US-10-237-656-5
10	80	54.1	137	14	US-10-237-656-3
11	79	53.4	194	14	US-10-295-074-46
12	79	53.4	285	14	US-10-295-074-11
13	78	52.7	50	9	US-09-943-548-8
14	78	52.7	50	14	US-10-339-522-8
15	78	52.7	158	14	US-10-297-942-14

Sequence 9, Appli
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Sequence 620, App
Sequence 1, Appli

285 14 US-10-295-074-9
287 14 US-10-295-074-15
24 14 US-10-128-711-110
51 9 US-09-848-834A-20
31 9 US-09-943-548-2
31 14 US-10-339-522-2
76 51.4
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158 14 US-10-297-942-2
15 9 US-09-862-849-2
15 9 US-09-785-215-4
15 10 US-09-405-986-1
15 14 US-10-204-362-4
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28 74 50.0
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US-09-848-834A-11
; Sequence 11, Application US/09848834A
; Patent No. US20020076416A1
; GENERAL INFORMATION:
; APPLICANT: Apton Corporation
; TITLE OF INVENTION: Chimeric Peptide Immunogens
; FILE REFERENCE: 1102865-0047
; CURRENT APPLICATION NUMBER: US/09/848,834A
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: 60/202,328
; PRIOR FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 11
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeric peptide consisting of amino acid sequence 830-844 of t
; OTHER INFORMATION: Tetanus toxoid precursor (Tetoxylisin) linked by a spacer to a
; OTHER INFORMATION: ino acid sequence 2-10 of the GnRH hormone
; NAME/KEY: MOD RES
; LOCATION: (1)..(11)
; OTHER INFORMATION: Amidated-glutamine
; NAME/KEY: MOD RES
; LOCATION: (28)..(28)
; OTHER INFORMATION: Amidated-glycine or glycineamide
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(15)
; OTHER INFORMATION: Amino acid sequence 830-844 of the Tetanus Toxoid Precursor
; OTHER INFORMATION: (Tetoxylisin)
; NAME/KEY: PEPTIDE
; LOCATION: (16)..(19)
; OTHER INFORMATION: Spacer peptide
; NAME/KEY: PEPTIDE
; LOCATION: (20)..(28)
; OTHER INFORMATION: Amino acid sequence 2-10 of the human GnRH hormone

ALIGNMENTS

RESULT 1

US-09-848-834A-11
; Sequence 11, Application US/09848834A
; Patent No. US20020076416A1
; GENERAL INFORMATION:
; APPLICANT: Apton Corporation
; TITLE OF INVENTION: Chimeric Peptide Immunogens
; FILE REFERENCE: 1102865-0047
; CURRENT APPLICATION NUMBER: US/09/848,834A
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: 60/202,328
; PRIOR FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 11
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeric peptide consisting of amino acid sequence 830-844 of t
; OTHER INFORMATION: Tetanus toxoid precursor (Tetoxylisin) linked by a spacer to a
; OTHER INFORMATION: ino acid sequence 2-10 of the GnRH hormone
; NAME/KEY: MOD RES
; LOCATION: (1)..(11)
; OTHER INFORMATION: Amidated-glutamine
; NAME/KEY: MOD RES
; LOCATION: (28)..(28)
; OTHER INFORMATION: Amidated-glycine or glycineamide
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(15)
; OTHER INFORMATION: Amino acid sequence 830-844 of the Tetanus Toxoid Precursor
; OTHER INFORMATION: (Tetoxylisin)
; NAME/KEY: PEPTIDE
; LOCATION: (16)..(19)
; OTHER INFORMATION: Spacer peptide
; NAME/KEY: PEPTIDE
; LOCATION: (20)..(28)
; OTHER INFORMATION: Amino acid sequence 2-10 of the human GnRH hormone

US-09-848-834A-11

Query Match 99.3%; Score 147; DB 9; Length 28;
 Best Local Similarity 100.0%; Pred. No. 8.4e-15;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QYIKANSKFIGITELGPSLHWSYGLRP 27
 Db 1 QYIKANSKFIGITELGPSLHWSYGLRP 27

RESULT 2

US-09-848-834A-19
 ; Sequence 19, Application US/09848834A
 ; Patent No. US20020076416A1

GENERAL INFORMATION:

APPLICANT: Aphton Corporation
 TITLE OF INVENTION: Chimeric Peptide Immunogens

FILE REFERENCE: 1102865-0047
 CURRENT APPLICATION NUMBER: US/09/848,834A

PRIOR FILING DATE: 2001-05-04

PRIOR APPLICATION NUMBER: 60/202,328

PRIOR FILING DATE: 2000-05-05

NUMBER OF SEQ ID NOS: 20

SOFTWARE: PatentIn version 3.0

SEQ ID NO 19

LENGTH: 46

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Chimeric peptide consisting of amino acid sequence 1-10 of human
 OTHER INFORMATION: GnRH linked by a spacer to amino acid sequence 830-844 of Tetanus
 OTHER INFORMATION: toxoid precursor (Tetoxylisin) linked by a spacer to amino acid
 OTHER INFORMATION: sequence 1-10 of GnRH

NAME/KEY: MOD_RES

LOCATION: (1)..(1)

OTHER INFORMATION: Pyroglutamic acid or 5-oxoproline

NAME/KEY: MOD_RES

LOCATION: (46)..(46)

OTHER INFORMATION: Amidated glycine or glycineamide

NAME/KEY: PEPTIDE

LOCATION: (1)..(10)

OTHER INFORMATION: Amino acid sequence 1-10 of the human GnRH hormone

NAME/KEY: PEPTIDE

LOCATION: (11)..(16)

OTHER INFORMATION: Spacer peptide

NAME/KEY: PEPTIDE

LOCATION: (17)..(31)

OTHER INFORMATION: Amino acid sequence 830-844 of the Tetanus toxoid precursor

NAME/KEY: PEPTIDE

LOCATION: (32)..(37)

OTHER INFORMATION: Spacer peptide

NAME/KEY: PEPTIDE

LOCATION: (38)..(46)

OTHER INFORMATION: Amino acid sequence 2-10 of the human GnRH hormone

US-09-848-834A-19

Query Match

Best Local Similarity 91.9%; Score 136; DB 9; Length 46;
 Matches 27; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

Qy 1 QYIKANSKFIGITEL--GPSLHWSYGLRP 27
 Db 17 QYIKANSKFIGITELSSGPSLHWSYGLRP 45

RESULT 3

US-10-076-674-7

; Sequence 7, Application US/10076674

; Publication No. US20030165478A1

GENERAL INFORMATION:

APPLICANT: Sokoll, Kenneth K.

; TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
 ; FILE REFERENCE: Immunogen Delivery System
 ; CURRENT APPLICATION NUMBER: US/10/076,674
 ; CURRENT FILING DATE: 2002-04-23
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: PatentIn version 3.1

SEQ ID NO 7

LENGTH: 27

TYPE: PRT

ORGANISM: Human

US-10-076-674-7

Query Match

Best Local Similarity 76.0%; Score 112.5; DB 14; Length 27;
 Matches 23; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

Qy 1 QYIKANSKFIGITELGPSLHWSYGLRP 27
 Db 3 QYIKANSKFIGITELE---HWSYGLRP 26

RESULT 4

US-10-355-161A-7

; Sequence 7, Application US/10355161A

; Publication No. US20040009897A1

GENERAL INFORMATION:

APPLICANT: Sokoll, Kenneth K.

; TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System

; FILE REFERENCE: Immunogen Delivery System

; CURRENT APPLICATION NUMBER: US/10/355,161A

; CURRENT FILING DATE: 2003-01-31

; PRIOR APPLICATION NUMBER: US 10/076674

; PRIOR FILING DATE: 2002-02-14

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: PatentIn version 3.1

SEQ ID NO 7

LENGTH: 27

TYPE: PRT

ORGANISM: Human

US-10-355-161A-7

Query Match

Best Local Similarity 76.0%; Score 112.5; DB 15; Length 27;
 Matches 23; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

Qy 1 QYIKANSKFIGITELGPSLHWSYGLRP 27
 Db 3 QYIKANSKFIGITELE---HWSYGLRP 26

RESULT 5

US-10-297-942-16

; Sequence 16, Application US/10297942

; Publication No. US20030185816A1

GENERAL INFORMATION:

APPLICANT: Ferring BV

; TITLE OF INVENTION: Solubilised Protein Vaccines

; FILE REFERENCE: P684450S0

; CURRENT APPLICATION NUMBER: US/10/297,942

; CURRENT FILING DATE: 2003-04-21

; PRIOR APPLICATION NUMBER: PCT/DK01/00431

; PRIOR FILING DATE: 2001-10-16

; PRIOR APPLICATION NUMBER: DK PA 2000 00966

; PRIOR FILING DATE: 2000-06-21

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: PatentIn version 3.1

SEQ ID NO 16

LENGTH: 158

TYPE: PRT

ORGANISM: Homo sapiens

US-10-297-942-16

Query Match

Best Local Similarity 55.4%; Score 82; DB 14; Length 158;

```
Best Local Similarity 89.5%; Pred. No. 0.00024;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QYKANSKFITIGTELGPSSL 19
Db 115 QYKANSKFITIGTELGDRL 133

RESULT 6
US-10-237-656-1
; Sequence 1, Application US/10237656
; Publication No. US20030152581A1
; GENERAL INFORMATION:
; APPLICANT: SAINT-REMY, Jean-Marie
; APPLICANT: JACQUEMIN, Marc
; TITLE OF INVENTION: COMPOUND AND METHOD FOR THE PREVENTION AND/OR THE TREATMENT OF AL
; FILE REFERENCE: 2002-0771/LC/01699
; CURRENT APPLICATION NUMBER: US/10/237,656
; CURRENT FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: 09/362,731
; PRIOR FILING DATE: 1999-07-29
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 2.1
; SEQ ID NO 1
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide
US-10-237-656-1

Query Match 55.1%; Score 81.5; DB 14; Length 31;
Best Local Similarity 61.3%; Pred. No. 5.1e-05;
Matches 19; Conservative 0; Mismatches 3; Indels 9; Gaps 1;

Qy 1 QYKANSKFITIGTELG-----PSLHWS 22
Db 1 QYKANSKFITIGTELGHKIKVLPGCHGS 31

RESULT 7
US-09-848-834A-12
; Sequence 12, Application US/09848834A
; Patent No. US20020076416A1
; GENERAL INFORMATION:
; APPLICANT: Aption Corporation
; TITLE OF INVENTION: Chimeric Peptide Immunogens
; FILE REFERENCE: 1102865-0047
; CURRENT APPLICATION NUMBER: US/09/848,834A
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: 60/202,328
; PRIOR FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeric peptide consisting of amino acid sequence 378-398 of the
; OTHER INFORMATION: Plasmodium falciparum CSP protein linked by a spacer to amino ac
; OTHER INFORMATION: id sequence 2-10 of the GnRH hormone
; NAME/KEY: MOD RES
; LOCATION: (1)_(1)
; OTHER INFORMATION: Amidated aspartic acid
; NAME/KEY: MOD RES
; LOCATION: (33)_(33)
; OTHER INFORMATION: Amidated glycine or glycineamide
; NAME/KEY: PEPTIDE
; LOCATION: (1)_(20)
; OTHER INFORMATION: Amino acid sequence 378-398 of the Malaria
; OTHER INFORMATION: (Plasmodium falciparum) circumsporozoite
; OTHER INFORMATION: (CSP) protein
```

```
; NAME/KEY: PEPTIDE
; LOCATION: (21)_(24)
; OTHER INFORMATION: Spacer peptide
; NAME/KEY: PEPTIDE
; LOCATION: (25)_(33)
; OTHER INFORMATION: Amino acid sequence 2-10 of the human GnRH hormone
US-09-848-834A-12

Query Match 55.1%; Score 81.5; DB 9; Length 33;
Best Local Similarity 66.7%; Pred. No. 5.5e-05;
Matches 16; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

Qy 4 KANSKFITIGTELGPSSLHWSYGLRP 27
Db 10 KASSVF-NVNSGPSLHWSYGLRP 32

RESULT 8
US-10-295-074-47
; Sequence 47, Application US/10295074
; Publication No. US20030185845A1
; GENERAL INFORMATION:
; APPLICANT: Pharmexa A/S
; TITLE OF INVENTION: NOVEL IMMUNOGENIC MIMETICS OF MULTIMER PROTEINS
; FILE REFERENCE: P1013DK00
; CURRENT APPLICATION NUMBER: US/10/295,074
; CURRENT FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 47
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: hTNF with inserted tetanus toxoid P2 and P30 epitopes
; NAME/KEY: MUTAGEN
; LOCATION: (110)_(130)
; OTHER INFORMATION: Tetanus toxoid P30 epitope
; FEATURE:
; NAME/KEY: MUTAGEN
; LOCATION: (131)_(145)
; OTHER INFORMATION: Tetanus toxoid P2 epitope
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (2)_(109)
; OTHER INFORMATION: hTNF amino acids 1-108
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (146)_(194)
; OTHER INFORMATION: hTNF amino acids 109-157
US-10-295-074-47

Query Match 54.7%; Score 81; DB 14; Length 194;
Best Local Similarity 76.2%; Pred. No. 0.00042;
Matches 16; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 QYKANSKFITIGTELGPSSLHW 21
Db 131 QYKANSKFITIGTELAEAXPW 151

RESULT 9
US-10-237-656-5
; Sequence 5, Application US/10237656
; Publication No. US20030152581A1
; GENERAL INFORMATION:
; APPLICANT: SAINT-REMY, Jean-Marie
; APPLICANT: JACQUEMIN, Marc
; TITLE OF INVENTION: COMPOUND AND METHOD FOR THE PREVENTION AND/OR THE TREATMENT OF
; FILE REFERENCE: 2002-0771/LC/01699
; CURRENT APPLICATION NUMBER: US/10/237,656
; CURRENT FILING DATE: 2002-09-10
```



```
; PRIOR APPLICATION NUMBER: 09/362,731
; PRIOR FILING DATE: 1999-07-29
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin Version 2.1
; SEQ ID NO 5
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide
US-10-237-656-5

Query Match          54.1%; Score 80; DB 14; Length 32;
Best Local Similarity 100.0%; Pred. No. 8.8e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QYIKANSKFIGITELG 16
Db 1 QYIKANSKFIGITELG 16

RESULT 10
US-10-237-656-3
; Sequence 3, Application US/10237656
; Publication No. US20030152581A1
; GENERAL INFORMATION:
; APPLICANT: SAINT-REMY, Jean-Marie
; APPLICANT: JACQUEMIN, Marc
; TITLE OF INVENTION: COMPOUND AND METHOD FOR THE PREVENTION AND/OR THE TREATMENT OF AL
; FILE REFERENCE: 2002-0771/LC/01699
; CURRENT APPLICATION NUMBER: US/10/237,656
; CURRENT FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: 09/362,731
; PRIOR FILING DATE: 1999-07-29
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin Version 2.1
; SEQ ID NO 3
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide
US-10-237-656-3

Query Match          54.1%; Score 80; DB 14; Length 137;
Best Local Similarity 100.0%; Pred. No. 0.00041;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QYIKANSKFIGITELG 16
Db 2 QYIKANSKFIGITELG 17

RESULT 11
US-10-295-074-46
; Sequence 46, Application US/10295074
; Publication No. US20030185845A1
; GENERAL INFORMATION:
; APPLICANT: Pharmexa A/S
; TITLE OF INVENTION: NOVEL IMMUNOGENIC MIMETICS OF MULTIMER PROTEINS
; FILE REFERENCE: P1013DK00
; CURRENT APPLICATION NUMBER: US/10/295,074
; CURRENT FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 46
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: hTNF with inserted tetanus toxoid P2 and P30 epitopes
; NAME/KEY: MUTAGEN
```

```
; LOCATION: (110)..(124)
; OTHER INFORMATION: Tetanus toxoid P2 epitope (SEQ ID NO: 2)
; FEATURE:
; NAME/KEY: MUTAGEN
; LOCATION: (125)..(145)
; OTHER INFORMATION: Tetanus toxoid P30 epitope (SEQ ID NO: 3)
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (2)..(109)
; OTHER INFORMATION: hTNF amino acids 1-108
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (145)..(194)
; OTHER INFORMATION: hTNF amino acids 109-157
US-10-295-074-46

Query Match          53.4%; Score 79; DB 14; Length 194;
Best Local Similarity 69.2%; Pred. No. 0.00084;
Matches 18; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 QYIKANSKFIGITELGPSLHWSYGLR 26
Db 110 QYIKANSKFIGITELFNFTVSPFLR 135

RESULT 12
US-10-295-074-11
; Sequence 11, Application US/10295074
; Publication No. US20030185845A1
; GENERAL INFORMATION:
; APPLICANT: Pharmexa A/S
; TITLE OF INVENTION: NOVEL IMMUNOGENIC MIMETICS OF MULTIMER PROTEINS
; FILE REFERENCE: P1013DK00
; CURRENT APPLICATION NUMBER: US/10/295,074
; CURRENT FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 11
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: 2 human IL5 monomers joined by P2 and P30 epitopes
US-10-295-074-11

Query Match          53.4%; Score 79; DB 14; Length 285;
Best Local Similarity 69.2%; Pred. No. 0.0013;
Matches 18; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 QYIKANSKFIGITELGPSLHWSYGLR 26
Db 135 QYIKANSKFIGITELFNFTVSPFLR 160

RESULT 13
US-09-943-548-8
; Sequence 8, Application US/09943548
; Patent No. US20020042364A1
; GENERAL INFORMATION:
; APPLICANT: Rittershaus, Charles W.
; APPLICANT: Thomas, Lawrence J.
; TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER TRANSFER PROTEIN (CETP) ACTIVITY
; FILE REFERENCE: TCS-411.1P US-1; TCS-411.1P US-2
; CURRENT APPLICATION NUMBER: US/09/943,548
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 08/432,483
; PRIOR FILING DATE: 1995-05-01
; PRIOR APPLICATION NUMBER: PCT/US96/06147
; PRIOR FILING DATE: 1996-05-01
; PRIOR APPLICATION NUMBER: 08/945,289
; PRIOR FILING DATE: 1997-10-17
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin version 3.1
```

```
; SEQ ID NO 8
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: vaccine peptide of the invention
US-09-943-548-8

Query Match          52.7%; Score 78; DB 9; Length 50;
Best Local Similarity 94.1%; Pred. No. 0.00028;
Matches 16; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 QYIKANSKFIGITELGP 17
   |||||
Db 2 QYIKANSKFIGITELFP 18
   |||||

RESULT 14
US-10-339-522-8
; Sequence 8, Application US/10339522
; Publication No. US20030108559A1
; GENERAL INFORMATION:
; APPLICANT: Rittershaus, Charles W.
; APPLICANT: Thomas, Lawrence J.
; TITLE OF INVENTION: MODULATION OF CHOLESTERYL ESTER TRANSFER PROTEIN (CETP) ACTIVITY
; FILE REFERENCE: TCS-411.1P US-3
; CURRENT APPLICATION NUMBER: US/10/339,522
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 08/432,483
; PRIOR FILING DATE: 1995-05-01
; PRIOR APPLICATION NUMBER: PCT/US96/06147
; PRIOR FILING DATE: 1996-05-01
; PRIOR APPLICATION NUMBER: 08/945,289
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 09/943,334
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: 09/943,548
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: vaccine peptide of the invention
US-10-339-522-8

Query Match          52.7%; Score 78; DB 14; Length 50;
Best Local Similarity 94.1%; Pred. No. 0.00028;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QYIKANSKFIGITELGP 17
   |||||
Db 2 QYIKANSKFIGITELFP 18
   |||||

RESULT 15
US-10-297-942-14
; Sequence 14, Application US/10297942
; Publication No. US20030185816A1
; GENERAL INFORMATION:
; APPLICANT: Ferring BV
; TITLE OF INVENTION: Solubilised Protein Vaccines
; FILE REFERENCE: P68445US0
; CURRENT APPLICATION NUMBER: US/10/297,942
; CURRENT FILING DATE: 2003-04-21
; PRIOR APPLICATION NUMBER: PCT/DK01/00431
; PRIOR FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: DK PA 2000 00966
; PRIOR FILING DATE: 2000-06-21
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
```

```
; SEQ ID NO 14
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-297-942-14

Query Match          52.7%; Score 78; DB 14; Length 158;
Best Local Similarity 81.0%; Pred. No. 0.00095;
Matches 17; Conservative 0; Mismatches 2; Indels 2; Gaps 1;

QY 1 QYIKANSKFIGITELGPSLHW 21
   |||||
Db 11 QYIKANSKFIGITEL--QLQW 29
   |||||

Search completed: March 10, 2004, 10:25:48
Job time : 22.0078 secs
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Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	147	99.3	28	5	AAU11422	AAU11422	Synthetic
2	136	91.9	46	5	AAU11430	AAU11430	Synthetic
3	119.5	80.7	47	2	AAR62723	AAR62723	LRRH-cont
4	112.5	76.0	27	2	AAR62701	AAR62701	LRRH-cont
5	112.5	76.0	27	7	ADD89947	ADD89947	LRRH-pept
6	86	58.1	750	3	AA926639	AA926639	Mutant hu
7	82	55.4	158	2	AAW81329	AAW81329	TNF2-4, a
8	82	55.4	158	5	ABB07281	ABB07281	Human TNF
9	82	55.4	693	3	AA926649	AA926649	Mutant hu
10	82	55.4	750	3	AA926630	AA926630	Mutant hu
11	82	55.4	750	3	AA926646	AA926646	Mutant hu
12	82	55.4	750	3	AA926641	AA926641	Mutant hu
13	81.5	55.1	31	3	AA926632	AA926632	Tetanus t
14	81.5	55.1	33	5	AAU11423	AAU11423	Synthetic
15	81	54.7	194	6	AAO30489	AAO30489	Human TNF
16	80.5	54.4	708	7	AAR62479	AAR62479	Modified
17	80	54.1	29	2	AAR63561	AAR63561	IGE CH4 r
18	80	54.1	32	3	AA926636	AA926636	Tetanus t
19	80	54.1	32	2	AA953389	AA953389	Universal
20	80	54.1	37	2	AAR65383	AAR65383	Universal
21	80	54.1	109	4	AAB50147	AAB50147	Growth di
22	80	54.1	137	3	AA926634	AA926634	Tetanus t
23	79	53.4	43	4	AAB49076	AAB49076	Amyloid b
24	79	53.4	43	4	AAB46177	AAB46177	Tetanus t
25	79	53.4	72	4	AAB46190	AAB46190	Tetanus t

or its analog.

Claim 11; Page 8; 43pp; English.

The invention relates to a synthetic immunogen for inducing specific antibodies against gonadotropin releasing hormone (GnRH) also known as luteinising hormone releasing hormone, LHRH) comprising a fusion peptide which comprises a promiscuous helper T-cell peptide epitope and immunogenic peptide epitope or its analogue. The synthetic immunogen is useful inducing an immune response against GnRH in an animal subject, and as such is useful as a contraceptive and in the treatment of diseases such as cancer (of the breast, uterus and other gynaecological cancer), endometriosis, uterine fibroids, benign prostatic hypertrophy and prostate cancer. The immunogen is effective in eliciting high and specific anti-GnRH antibody titres. The present sequence is a synthetic immunogen of the invention

Sequence 28 AA;

Query Match 99.3%; Score 147; DB 5; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.1e-15;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYIKANSKFIGITELGPSLHWSYGLRP 27
DB 1 QYIKANSKFIGITELGPSLHWSYGLRP 27

RESULT 2
AAU11430
ID AAU11430 standard; peptide; 46 AA.
AC AAU11430;
XX
DT 12-MAR-2002 (first entry)
DE Synthetic immunogen peptide 11.
XX Gonadotropin releasing hormone; GnRH; synthetic immunogen;
KW luteinising hormone releasing hormone; LHRH; contraceptive;
KW promiscuous helper T-cell peptide epitope; immunogenic peptide epitope;
KW breast cancer; uterine cancer; gynaecological cancer; endometriosis;
KW uterine fibroid; benign prostatic hypertrophy; prostate cancer.
XX Clostridium tetani.
OS Mammalia.
OS Synthetic.
OS Chimeric.
XX

Key Location/Qualifiers
FT Peptide 1..10
FT /note= "Gonadotropin releasing hormone epitope (1..10 aa)"
FT Misc-difference 1
FT /label= OTHER
FT /note= "Other= Pyro-glutamic acid or 5-oxo proline"
FT Peptide 11..16
FT /note= "Spacer peptide"
FT Peptide 17..31
FT /note= "Tetanus toxoid (830-844 aa)"
FT Peptide 32..37
FT /note= "Spacer peptide"
FT Peptide 38..46
FT /note= "Gonadotropin releasing hormone epitope (2-10 aa)"
FT Modified-site 46
FT /note= "Amidated glycine or glycineamide"
XX
XX WO200185763-A2.
PN
XX 15-NOV-2001.
PD
XX 04-MAY-2001; 2001WO-US014363.
PF

05-MAY-2000; 2000US-0202328P.
(APHT-) APHTON CORP.
Grimes S, Michaeli D, Stevens VC;
WPI; 2002-049440/06.
Novel synthetic immunogen for inducing immune response against gonadotropin releasing hormone, comprises fusion peptide having promiscuous helper T-cell peptide epitope and immunogenic peptide epitope or its analog.
Claim 11; Page 12; 43pp; English.

The invention relates to a synthetic immunogen for inducing specific antibodies against gonadotropin releasing hormone (GnRH) also known as luteinising hormone releasing hormone, LHRH) comprising a fusion peptide which comprises a promiscuous helper T-cell peptide epitope and immunogenic peptide epitope or its analogue. The synthetic immunogen is useful inducing an immune response against GnRH in an animal subject, and as such is useful as a contraceptive and in the treatment of diseases such as cancer (of the breast, uterus and other gynaecological cancer), endometriosis, uterine fibroids, benign prostatic hypertrophy and prostate cancer. The immunogen is effective in eliciting high and specific anti-GnRH antibody titres. The present sequence is a synthetic immunogen of the invention

Sequence 46 AA;

Query Match 91.9%; Score 136; DB 5; Length 46;
Best Local Similarity 93.1%; Pred. No. 1.8e-13;
Matches 27; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 QYIKANSKFIGITEL-GPSLHWSYGLRP 27
DB 17 QYIKANSKFIGITELSGPSLWSYGLRP 45

RESULT 3
AAS62723
ID AAR62723 standard; peptide; 47 AA.
XX AAR62723;
XX 25-MAR-2003 (revised)
DT 17-SEP-1995 (first entry)
XX LHRH-containing immunogenic peptide.
XX Helper T cell epitope; universal immune stimulator; invasive; haptens; vaccine; LHRH; luteinising hormone releasing hormone; prostate; toxin; androgen-dependent carcinoma; antitumour; infertility; tetanus toxin.
XX Synthetic.
XX Key Location/Qualifiers
FT Domain 1..16 "invasin domain"
FT /note= "invasin domain"
FT Domain 19..35
FT /note= "tetanus toxin helper T cell epitope"
FT Domain 38..47
FT /note= "LHRH haptens"
XX
XX WO9425060-A1.
PN
XX 10-NOV-1994.
PD
XX 28-APR-1994; 94WO-US004832.
PF
XX 27-APR-1993; 93US-00057166.
PD
XX 14-APR-1994; 94US-00229275.
PF

```

XX (LADD/) LADD A E.
PA (WANG/) WANG C Y.
PA (ZAMB/) ZAMB T.
XX
PI Ladd AE, Wang CY, Zamb T;
XX
DR WPI; 1994-357910/44.
XX
XX Immunogenic luteinising hormone releasing hormone peptide(s) - that
PT suppress LHRH activity in males and females.
XX
PS Claim 8; Page 88; 213pp; English.
XX
CC Synthetic immunogenic peptides are provided in which a universal immune
CC stimulator is linked to a peptide or protein haptens containing B cell
CC and/or cytotoxic T lymphocyte epitopes, giving a product which causes
CC potent immune responses to the coupled peptide or protein. The stimulator
CC consists of (A) a promiscuous helper T cell epitope (Th) which elicits an
CC immune response to the coupled peptide in members of a heterogeneous
CC population expressing diverse HLA phenotypes, and (B) an adjuvant peptide
CC sequences from the invasive protein of Yersinia. Spacer amino acid
CC sequences (e.g. Gly-Gly) can be provided between the invasin and Th
CC domains and between the immune stimulator and haptens components. When the
CC haptens is LHRH, then optionally the invasin domain can be omitted from
CC the immune stimulator component. The present sequence represents an LHRH-
CC containing immunogenic peptide as above which can be used as a potent
CC vaccine for treating e.g. prostatic hyperplasia, androgen-dependent
CC carcinoma, prostatic carcinoma, testicular carcinoma, endometriosis,
CC benign uterine tumours, recurrent functional ovarian cysts, (severe)
CC premenstrual syndrome or oestrogen-dependent breast cancer, or for
CC induction of infertility. (Updated on 25-MAR-2003 to correct FN field.)
XX
SQ Sequence 47 AA;
Query Match 80.7%; Score 119.5; DB 2; Length 47;
Best Local Similarity 88.9%; Pred. No. 6.7e-11;
Matches 24; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 QYIKANSKFIGITELGSLHWSYGLRP 27
Db 21 QYIKANSKFIGITELGSGE-HWSYGLRP 46

RESULT 4
AAR62701
ID AAR62701 standard; peptide; 27 AA.
XX
AC AAR62701;
XX
DT 25-MAR-2003 (revised)
DT 10-SEP-1995 (first entry)
XX
DE LHRH-containing immunogenic peptide.
XX
XX Helper T cell epitope; universal immune stimulator; invasin; haptens;
XX vaccine; LHRH; luteinising hormone releasing hormone; prostate;
XX androgen-dependent carcinoma; antitumour; infertility; tetanus toxin.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH Domain 1..17
FT Domain /note= "tetanus toxin helper T cell epitope"
FT Domain 18..27
FT Domain /note= "LHRH haptens"
XX
XX WO9425060-A1.
XX
XX 10-NOV-1994.
XX
XX 28-APR-1994; 94WO-US004832.
XX

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PR 27-APR-1993; 93US-00057166.
PR 14-APR-1994; 94US-00229275.
XX
PA (LADD/) LADD A E.
PA (WANG/) WANG C Y.
PA (ZAMB/) ZAMB T.
XX
PI Ladd AE, Wang CY, Zamb T;
XX
XX WPI; 1994-357910/44.
XX
XX Immunogenic luteinising hormone releasing hormone peptide(s) - that
PT suppress LHRH activity in males and females.
XX
XX Claim 8, 12; Page 84; 213pp; English.
XX
CC Synthetic immunogenic peptides are provided in which a universal immune
CC stimulator is linked to a peptide or protein haptens containing B cell
CC and/or cytotoxic T lymphocyte epitopes, giving a product which causes
CC potent immune responses to the coupled peptide or protein. The stimulator
CC consists of (A) a promiscuous helper T cell epitope (Th) which elicits an
CC immune response to the coupled peptide in members of a heterogeneous
CC population expressing diverse HLA phenotypes, and (B) an adjuvant peptide
CC sequences from the invasive protein of Yersinia. Spacer amino acid
CC sequences (e.g. Gly-Gly) can be provided between the invasin and Th
CC domains and between the immune stimulator and haptens components. When the
CC haptens is LHRH, then optionally the invasin domain can be omitted from
CC the immune stimulator component. The present sequence represents an LHRH-
CC containing immunogenic peptide as above which can be used
CC as a potent vaccine for treating e.g. prostatic hyperplasia, androgen-
CC dependent carcinoma, prostatic carcinoma, testicular carcinoma,
CC endometriosis, benign uterine tumours, recurrent functional ovarian
CC cysts, (severe) premenstrual syndrome or oestrogen-dependent breast
CC cancer, or for induction of infertility. This sequence is particularly
CC preferred. (Updated on 25-MAR-2003 to correct FN field.)
XX
SQ Sequence 27 AA;
Query Match 76.0%; Score 112.5; DB 2; Length 27;
Best Local Similarity 85.2%; Pred. No. 4.4e-10;
Matches 23; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

QY 1 QYIKANSKFIGITELGSLHWSYGLRP 27
Db 3 QYIKANSKFIGITELB--HWSYGLRP 26

RESULT 5
ADD89947
ID ADD89947 standard; protein; 27 AA.
XX
AC ADD89947;
XX
DT 29-JAN-2004 (first entry)
XX
DE LHRH peptide used in immunostimulant complex for prostate cancer vaccine.
XX
XX Immunostimulant; vaccine; human; immunogen; LHRH; immunotherapy;
XX prostate cancer.
XX
XX Synthetic.
XX
XX Homo sapiens.
XX
XX WO2003068169-A2.
XX
XX 21-AUG-2003.
XX
XX 14-FEB-2003; 2003WO-US004711.
XX
XX 14-FEB-2002; 2002US-00076674.
XX
XX 31-JAN-2003; 2003US-00076674.
XX
XX (UNBI-) UNITED BIOMEDICAL INC.
PA

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Sokoll KK;

WPI; 2003-778990/73.

**Stabilized immunostimulating complex, useful for vaccination, e.g.
against human immune deficiency viruses, comprises cationic peptide
immunogen and anionic oligonucleotide.**

Claim 17; SEQ ID NO 7; 159pp; English.

The present sequence is that of a synthetic immunogenic peptide derived from human LHRH. This is an example of peptides that can be used in claimed immunostimulatory complexes of the invention that are specifically adapted to act as adjuvant and as peptide immunogen stabiliser. The complexes comprise a CpG oligonucleotide and a biologically active peptide immunogen. The complex is particulate and can efficiently present peptide immunogens to the cells of the immune system to produce an immune response. The complexes may be prepared with various ratios of peptides to CpG oligonucleotides to provide different physical properties, such as the size of the microparticle. An immunostimulatory complex comprising the present LHRH derived peptide can be used in a vaccine for prostate cancer.

Sequence 27 AA;

Query Match 76.0%; Score 112.5; DB 7; Length 27;
Best Local Similarity 85.2%; Pred. No. 4.4e-10;
Matches 23; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

QY 1 QYIKANSKFIGITELGPSLHWYSGLRP 27

DB 3 QYIKANSKFIGITELS---HWSYGRLP 26

RESULT 6

AAY92639 standard; protein; 750 AA.

ID AAY92639

AC AAY92639;

DT 10-AUG-2000 (first entry)

XX Mutant human prostate specific membrane antigen construct, hPSM5.1.

DE Prostate specific membrane antigen; immunogenized construct; mutant;

KW vaccination; cytotoxic T-lymphocyte immunity; breast cancer;

XN prostate cancer; cell-associated peptide antigen; foreign epitope.

XX Homo sapiens.

OS Synthetic.

PH Key Location/Qualifiers

FT Peptide 21..41 /label= P30 /note= "foreign epitope"

ET Peptide 305..319 /label= P2 /note= "foreign epitope"

FO WO200020027-A2.

FN 13-APR-2000.

PB 05-OCT-1999; 99WO-DK000525.

PP 05-OCT-1998; 98DK-00001261.

PR 20-OCT-1998; 98US-0105011P.

PA (MEBI-) M & E BIOTECH AS.

PI Steinaas L, Mouritsen S, Nielsen KG, Haaning J, Leach D, Dalum I;

XX

Sokol KK;

WPI; 2000-349917/30.

Inducing immune responses to weakly immunogenic, tumor associated peptide antigens for the treatment of breast and prostate cancer.

Example 1; Page; 220pp; English.

AAY92627-49 are mutant immunogenized human prostate specific membrane antigen (PSM) constructs, which contain foreign epitopes (P2 and/or P30). The immunogenic analogues of PSM can be used in the claimed method as an autovaccine to induce a CTL response. Subdominant CTL epitopes, antibody binding regions and cysteine residues involved in disulfide bonds are preserved in the immunogenized forms. The method is used for inducing immune responses against weakly immunogenic cell-associated peptide antigens (PA) such as those associated with cancers (self-proteins), e.g. human prostate specific membrane antigen (PSM), heregulin 2 (Her2) and/or fibroblast growth factor 8b (FGF8b). The method comprises effecting simultaneous presentation by antigen producing cells (APCs) of the animals' immune system of: (1) at least 1 CTL cytototoxic T-lymphocyte group derived from the PA and/or at least 1 B-cell group derived from the cell-associated PA; and (2) at least 1 first T helper cell group which is foreign to the animal. Analogues of human FPM, human Her2 and human/murine FGF8b comprising a substantial part of all known and predicted CTL and B-cell epitopes of the respective PA and including at least one foreign T helper epitope or also claimed. The method is used to treat prostate, prostate/breast or breast cancer when the PA is human PSM, FGF8b and Her2, respectively. Note: This sequence was constructed from the wild type human PSM (AAY92619), which appears on pages 184-187 of the specification

Sequence 750 AA;

Query Match 58.1%; Score 86; DB 3; Length 750;
Best Local Similarity 70.4%; Pred. No. 0.00023;
Matches 19; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 QYIKANSKFIGITELGPSLHWYSGLRP 27

DB 305 QYIKANSKFIGITELRGSLKPYNVGP 331

RESULT 7

AAY91329 standard; protein; 158 AA.

ID AAY91329

AC AAW81329;

DT 21-APR-1999 (first entry)

XX TNF2-4, a TNF-alpha analogue.

DE Human tumour necrosis factor-alpha; TNF-alpha; TNF-alpha analogue;

KW vaccine; rheumatoid arthritis; Crohn's disease; ulcerative colitis;

XN cancer; disseminated sclerosis; diabetes; psoriasis; osteoporosis;

XX asthma.

OS Synthetic.

OS Homo sapiens.

PN W09846642-A1.

PD 22-OCT-1998.

PF 15-APR-1998; 98WC-DK000157.

PP 15-APR-1997; 97DU-00000418.

PR 24-APR-1997; 97US-0044187P.

XX (FERRE) FARM LAB FERRING AS.

PA Jensen MR, Mouritsen S, Elsen H, Dalum I;

PI

DR WPI; 1998-594561/50.
 DR N-PSDB; AAV68418.
 XX Modified human tumour necrosis factor-alpha - comprises immunodominant T
 PT cell epitope, useful in vaccines to treat or prevent TNF-associated
 PT diseases, e.g. cancer.
 XX
 XX
 PS Example 1; Page 69-70; 134pp; English.
 CC The present sequence represents a modified human tumour necrosis factor-
 CC alpha (TNF-alpha) analogue. The analogues have no residual TNF activity
 CC and are immunogenic in a large proportion of the human population (by
 CC using promiscuous epitopes). The TNF-alpha analogue is able to generate,
 CC in humans, neutralizing antibodies to wild-type human TNF alpha, has at
 CC least one fragment of TNF substituted by a peptide containing an
 CC immunodominant T-cell epitope, and at least one TNF-alpha B-cell epitope.
 CC The substitution causes a significant change in the amino acid sequence
 CC of any one of the strands in the front beta-sheet, any of the connecting
 CC loops or any of the B', I or D strands in the back beta-sheet. The TNF-
 CC alpha analogues are used as vaccines for treatment or prevention of
 CC diseases associated with excessive release or activity of TNF-alpha, e.g.
 CC rheumatoid arthritis, Crohn's disease, ulcerative colitis, cancer of any
 CC sort, disseminated sclerosis, diabetes, psoriasis, osteoporosis and
 CC asthma
 XX
 SQ Sequence 158 AA;
 Query Match 55.4%; Score 82; DB 2; Length 158;
 Best Local Similarity 89.5%; Pred. No. 0.00017;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 QYIKANSKFIGHTELGDSL 19
 DB 115 QYIKANSKFIGHTELGDSL 133
 RESULT 8
 ID ABB07281 standard; protein; 158 AA.
 XX
 AC ABB07281;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Human TNF-alpha analogue TNF2-4.
 XX
 KW TNF-alpha; pharmaceutical; vaccine; self-protein; tumour necrosis factor;
 KW cetylpyridinium chloride; immunisation; antiinflammatory; antirheumatic;
 KW antiarthritic; antiulcer; cytostatic; antidiabetic; antipsoriatic;
 KW antiasthmatic; immunomodulator; neuroprotective; osteoprotective; human;
 TNF2-4.
 XX
 OS Homo sapiens.
 XX
 FN WO200197837-A1.
 XX
 PD 27-DEC-2001.
 XX
 XX 20-JUN-2001; 2001WO-DK000431.
 XX
 XX 21-JUN-2000; 2000DK-00000965.
 PR
 XX (FERR) FERRING BV.
 PA
 XX Olesen OF, Balchen T, Bouman MHEM;
 PI
 XX WPI; 2002-114542/15.
 DR
 DR N-PSDB; ABA94391.
 XX
 XX Novel vaccine composition for prevention/treatment of self-protein-
 PT mediated pathology such as cancer, diabetes and asthma, comprises
 PT modified immunogenic self-protein and surfactant capable of acting as
 PT solubilizer.

XX Claim 21; Page 46-47; 55pp; English.
 PS
 CC The invention provides a pharmaceutical vaccine composition (I) for the
 CC prevention or treatment of a self-protein-mediated pathology. The
 CC composition comprises at least one modified immunogenic self-protein
 CC (selected from modified TNF-alpha proteins) and a surfactant capable of
 CC acting as a solubilizer. (I) is useful for preventing or treating a self
 CC -protein-mediated pathology such as an inflammatory disease, rheumatoid
 CC arthritis, an inflammatory bowel disease (ulcerative colitis or Crohn's
 CC disease), cancer, cachexia, multiple sclerosis, diabetes, psoriasis,
 CC osteoporosis or asthma. (I) is useful for inducing autoantibodies to a
 CC self-protein such as TNF (tumour necrosis factor)-alpha in a human
 CC subject. (I) comprising cetylpyridinium chloride as a component is useful
 CC for immunisation of a human subject or for treatment of a human
 CC inflammatory disease. The present sequence represents a human TNF-alpha
 CC analogue TNF2-4
 XX
 SQ Sequence 158 AA;
 Query Match 55.4%; Score 82; DB 5; Length 158;
 Best Local Similarity 89.5%; Pred. No. 0.00017;
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 QYIKANSKFIGHTELGDSL 19
 DB 115 QYIKANSKFIGHTELGDSL 133
 RESULT 9
 ID AAY92649 standard; protein; 693 AA.
 XX
 AC AAY92649;
 XX
 DT 10-AUG-2000 (first entry)
 XX
 DE Mutant human PSM antigen splice variant construct, hPSM'10.3.
 XX
 KW Prostate specific membrane antigen; immunogenized construct; mutant;
 KW vaccination; cytotoxic T-lymphocyte immunity; breast cancer; PSM;
 KW prostate cancer; cell-associated peptide antigen; foreign epitope.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Peptide 153..173
 FT /label= P30
 FT /note= "foreign epitope"
 FT Peptide 617..631
 FT /label= P2
 FT /note= "foreign epitope"
 XX
 PN WO200020027-A2.
 XX
 PD 13-APR-2000.
 XX
 XX 05-OCT-1999; 99WO-DK000525.
 XX
 XX 05-OCT-1998; 98DK-00001261.
 PR
 PR 20-OCT-1998; 98US-0105011P.
 XX
 XX (MEBI-) M & E BIOTECH AS.
 PA
 XX Steinaa I, Mouritsen S, Nielsen KG, Haaning J, Leach D, Dalum I;
 PI Gautam A, Birk P, Karlsson G;
 XX
 XX WPI; 2000-349917/30.
 DR
 XX Inducing immune responses to weakly immunogenic, tumor associated peptide
 PT antigens for the treatment of breast and prostate cancer.
 PT
 XX

```

PS Example 1; Page: 220pp; English.
XX
CC AAY92627-49 are mutant immunogenized human prostate specific membrane
CC antigen (PSM) constructs, which contain foreign epitopes (P2 and/or P30).
CC The immunogenic analogues of PSM can be used in the claimed method as an
CC autovaccine to induce a CTL response. Subdominant CTL epitopes, antibody
CC binding regions and cysteine residues involved in disulfide bonds are
CC preserved in the immunogenized forms. The method is used for inducing
CC immune responses against weakly immunogenic cell-associated peptide
CC antigens (PA) such as those associated with cancers (self-proteins), e.g.
CC human prostate specific membrane antigen (PSM), heregulin 2 (Her2) and/or
CC fibroblast growth factor 8b (FGF8b). The method comprises effecting
CC simultaneous presentation by antigen producing cells (APCs) of the
CC animals immune system of: (1) at least 1 CTL (cytotoxic T-lymphocyte)
CC group derived from the PA and/or at least 1 B-cell group derived from the
CC cell-associated PA; and (2) at least 1 first T helper cell group which is
CC foreign to the animal. Analogues of human PSM, human Her2 and
CC human/murine FGF8b comprising a substantial part of all known and
CC predicted CTL and B-cell epitopes of the respective PA and including at
CC least one foreign T helper epitope are also claimed. The method is used
CC to treat prostate, prostate/breast or breast cancer when the PA is human
CC PSM, FGF8b and Her2, respectively. Note: This sequence was constructed
CC from the wild type human PSM (AAY92619), which appears on pages 184-187
CC of the specification
XX
SQ Sequence 693 AA;
Query Match 55.4%; Score 82; DB 3; Length 693;
Best Local Similarity 70.4%; Pred. No. 0.00087;
Matches 19; Conservative 0; Mismatches 4; Indels 4; Gaps 1;

QY 1 QYIKANSKFIGITEL-----GPSLHWSY 23
DB 617 QYIKANSKFIGITELHVIYAPSSHNY 643

RESULT 10
AAY92630
ID AAY92630 standard; protein; 750 AA.
XX
AC AAY92630;
XX
DT 10-AUG-2000 (first entry)
XX
DE Mutant human prostate specific membrane antigen construct, hPSM10.1.
XX
KW Prostate specific membrane antigen; immunogenized construct; mutant;
KW vaccination; cytotoxic T-lymphocyte immunity; breast cancer;
KW prostate cancer; cell-associated peptide antigen; foreign epitope.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 21..41
FT /label= P30
FT /note= "foreign epitope"
FT Peptide 674..688
FT /label= P2
FT /note= "foreign epitope"
XX
XX WO200020027-A2.
XX
PN 13-APR-2000.
XX
PD 05-OCT-1999; 99WO-DK000525.
XX
PF 05-OCT-1998; 98DK-00001261.
PR 20-OCT-1998; 98US-0105011P.
XX
XX (MEBI-) M & E BIOTECH AS.
XX
PI Steinaa L, Mouritsen S, Nielsen KG, Haaning J, Leach D, Dalum I;

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PI Gautam A, Birk P, Karlsson G;
XX
DR WF; 2000-349917/30.
XX
FT Inducing immune responses to weakly immunogenic, tumor associated peptide
FT antigens for the treatment of breast and prostate cancer.
XX
XX Example 1; Page: 220pp; English.
XX
CC AAY92627-49 are mutant immunogenized human prostate specific membrane
CC antigen (PSM) constructs, which contain foreign epitopes (P2 and/or P30).
CC The immunogenic analogues of PSM can be used in the claimed method as an
CC autovaccine to induce a CTL response. Subdominant CTL epitopes, antibody
CC binding regions and cysteine residues involved in disulfide bonds are
CC preserved in the immunogenized forms. The method is used for inducing
CC immune responses against weakly immunogenic cell-associated peptide
CC antigens (PA) such as those associated with cancers (self-proteins), e.g.
CC human prostate specific membrane antigen (PSM), heregulin 2 (Her2) and/or
CC fibroblast growth factor 8b (FGF8b). The method comprises effecting
CC simultaneous presentation by antigen producing cells (APCs) of the
CC animals immune system of: (1) at least 1 CTL (cytotoxic T-lymphocyte)
CC group derived from the PA and/or at least 1 B-cell group derived from the
CC cell-associated PA; and (2) at least 1 first T helper cell group which is
CC foreign to the animal. Analogues of human PSM, human Her2 and
CC human/murine FGF8b comprising a substantial part of all known and
CC predicted CTL and B-cell epitopes of the respective PA and including at
CC least one foreign T helper epitope are also claimed. The method is used
CC to treat prostate, prostate/breast or breast cancer when the PA is human
CC PSM, FGF8b and Her2, respectively. Note: This sequence was constructed
CC from the wild type human PSM (AAY92619), which appears on pages 184-187
CC of the specification
XX
SQ Sequence 750 AA;
Query Match 55.4%; Score 82; DB 3; Length 750;
Best Local Similarity 70.4%; Pred. No. 0.00095;
Matches 19; Conservative 0; Mismatches 4; Indels 4; Gaps 1;

QY 1 QYIKANSKFIGITEL-----GPSLHWSY 23
DB 674 QYIKANSKFIGITELHVIYAPSSHNY 700

RESULT 11
AAY92646
ID AAY92646 standard; protein; 750 AA.
XX
AC AAY92646;
XX
DT 10-AUG-2000 (first entry)
XX
DE Mutant human prostate specific membrane antigen construct, hPSM10.3.
XX
KW Prostate specific membrane antigen; immunogenized construct; mutant;
KW vaccination; cytotoxic T-lymphocyte immunity; breast cancer;
KW prostate cancer; cell-associated peptide antigen; foreign epitope.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 210..230
FT /label= P30
FT /note= "foreign epitope"
FT Peptide 674..688
FT /label= P2
FT /note= "foreign epitope"
XX
XX WO200020027-A2.
XX
PN 13-APR-2000.
XX
PD 05-OCT-1999; 99WO-DK000525.
XX
PF

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XX 05-OCT-1998; 98DK-00001261.
PR 20-OCT-1998; 98US-0105011P.
XX
XX (MEBI-) M & E BIOTECH AS.
XX
XX Steinaa L, Mouritsen S, Nielsen KG, Haaning J, Leach D, Dalum I;
PI Gautam A, Birk P, Karlsson G;
XX
XX WPI; 2000-349917/30.
XX
XX Inducing immune responses to weakly immunogenic, tumor associated peptide
PT antigens for the treatment of breast and prostate cancer.
XX
XX Example 1; Page; 220pp; English.
XX
XX AAY92627-49 are mutant immunogenized human prostate specific membrane
CC antigen (PSM) constructs, which contain foreign epitopes (P2 and/or P30).
CC The immunogenic analogues of PSM can be used in the claimed method as an
CC autovaccine to induce a CTL response. Subdominant CTL epitopes, antibody
CC binding regions and cysteine residues involved in disulfide bonds are
CC preserved in the immunogenized forms. The method is used for inducing
CC immune responses against weakly immunogenic cell-associated peptide
CC antigens (PA) such as those associated with cancers (self-proteins), e.g.
CC human prostate specific membrane antigen (PSM), heregulin 2 (Her2) and/or
CC fibroblast growth factor 8b (FGF8b). The method comprises effecting
CC simultaneous presentation by antigen producing cells (APCs) of the
CC group derived from the PA and/or at least 1 CTL (cytotoxic T-lymphocyte)
CC cell-associated PA; and (2) at least 1 first T helper cell group which is
CC foreign to the animal. Analogues of human PSM, human Her2 and
CC human/murine FGF8b comprising a substantial part of all known and
CC predicted CTL and B-cell epitopes of the respective PA and including at
CC least one foreign T helper epitope are also claimed. The method is used
CC to treat prostate, prostate/breast or breast cancer when the PA is human
CC PSM, FGF8b and Her2, respectively. Note: This sequence was constructed
CC from the wild type human PSM (AAY92619), which appears on pages 184-187
CC of the specification
XX
XX Sequence 750 AA;
XX
XX Query Match 55.4%; Score 82; DB 3; Length 750;
XX Best Local Similarity 70.4%; Pred. No. 0.00095;
XX Matches 19; Conservative 0; Mismatches 4; Indels 4; Gaps 1;
XX
XX 1 QYIKANSKFIGITEL---GPSLHWSY 23
XX 674 QYIKANSKFIGITELHVIYAPSSHNY 700
XX
XX RESULT 12
XX AAY92641
XX ID AAY92641 standard; protein; 750 AA.
XX
XX AC AAY92641;
XX
XX 10-AUG-2000 (first entry)
XX
XX Mutant human prostate specific membrane antigen construct, hPSM10.0.
XX
XX Prostate specific membrane antigen; immunogenized construct; mutant;
XX vaccination; Cytotoxic T-lymphocyte immunity; breast cancer;
XX prostate cancer; cell-associated peptide antigen; foreign epitope.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Peptide 674..688
XX /label= P2
XX /note= "foreign epitope"
XX
XX WO200020027-A2.

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OS Synthetic.
XX WO200006694-A2.
XX
XX 10-FEB-2000.
XX
XX 20-JUL-1999; 99WO-BE000092.
XX
XX 30-JUL-1998; 98EP-00870167.
XX
XX (UNIO ) UCB SA.
XX
XX Saint-Remy J, Jacquemin M;
XX
XX WPI; 2000-422470/36.
XX
XX New compound for prevention and treatment of allergies comprises at least
XX one allergenic determinant recognized by a B cell and at least
XX one antigenic determinant which does not trigger T cell activation.
XX
XX Claim 8; Page 35; 50pp; English.
XX
XX The present invention describes a compound (I) for the prevention and/or
XX treatment of allergy. The compound comprises at least one allergen
XX antigenic determinant (i) recognised by a B cell or an antibody secreted
XX by a B cell of a non-atopic individual and at least one antigenic
XX determinant (ii) different from the allergen that triggers T cell
XX activation. (i) has antiallergic, antisthmatic, antiinflammatory,
XX dermatological and immunosuppressive activities, and can be used in a
XX vaccine. (ii) may be used in a pharmaceutical or cosmetic medicament to
XX treat and/or prevent allergies or a disease of allergic origin,
XX especially hypersensitivities. These include rhinitis, sinusitis,
XX bronchial asthma, atopic dermatitis, some forms of acute and chronic
XX urticaria, gastro-intestinal syndromes associated with the ingestion of
XX food allergens, oro-pharyngeal syndromes, anaphylactic reactions
XX associated with drug hypersensitivities and/or a mixture of these. The
XX use of (i) in the treatment of allergic conditions avoids the need for
XX drug treatment, which often causes undesirable side-effects. Also, prior
XX art drug therapies alleviate symptoms, but do not influence their causes,
XX however (i) actually combats the cause of an allergic reaction. The
XX present sequence represents a specifically claimed compound peptide
XX sequence from the present invention
XX
XX Sequence 31 AA;
XX
XX Query Match 55.1%; Score 81.5; DB 3; Length 31;
XX Best Local Similarity 61.3%; Pred. No. 3.2e-05;
XX Matches 19; Conservative 0; Mismatches 3; Indels 9; Gaps 1;
XX
XX Qy 1 QYIKANSKFIGITELG-----PSLHWS 22
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX Db 1 QYIKANSKFIGITELGGHETKKVLVPGCHG 31
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX
XX RESULT 14
XX AAU11423
XX ID AAU11423 standard; peptide; 33 AA.
XX
XX AC AAU11423;
XX
XX 12-MAR-2002 (first entry)
XX
XX Synthetic immunogen peptide 4.
XX
XX Gonadotrophin releasing hormone; GnRH; synthetic immunogen;
XX luteinising hormone releasing hormone; LHRH; contraceptive;
XX promiscuous helper T-cell peptide epitope; immunomimic peptide epitope;
XX breast cancer; uterine cancer; gynaecological cancer; endometriosis;
XX uterine fibroid; benign prostatic hypertrophy; prostate cancer.
XX
XX Plasmodium falciparum.
XX Mammalia.
XX Synthetic.
XX
XX RESULT 15
XX AAO30489
XX ID AAO30489 standard; protein; 194 AA.
XX
XX AC AAO30489;
XX
XX 22-SEP-2003 (first entry)
XX
XX Human TNFalpha variant, TNF34-P30-P2.
XX
XX Multimeric protein; interleukin 5; IL5; TNFalpha; inflammatory disease;
XX tumour necrosis factor alpha; gene therapy; arthritis; human; mutant;
XX mutein; variant; tetanus toxoid; epitope.
XX
XX Homo sapiens.
XX Unidentified.
XX
OS

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OS Chimeric.
XX Key Location/Qualifiers
XX Peptide 1..20
XX /note= "Malaria CSP protein (378-398 aa)"
XX Peptide 21..24
XX /note= "Spacer peptide"
XX Peptide 25..33
XX /note= "Gonadotrophin releasing hormone epitope"
XX Modified-site 33
XX /note= "Amidated glycine or glycineamide"
XX
XX WO200185763-A2.
XX
XX 15-NOV-2001.
XX
XX 04-MAY-2001; 2001WO-US014363.
XX
XX 05-MAY-2000; 2000US-0203328P.
XX
XX (APHT-) APHTON CORP.
XX
XX Grimes S, Michaeli D, Stevens VC;
XX WPI; 2002-049440/06.
XX
XX Novel synthetic immunogen for inducing immune response against
XX gonadotropin releasing hormone, comprises fusion peptide having
XX promiscuous helper T-cell peptide epitope and immunomimic peptide epitope
XX or its analog.
XX
XX Claim 11; Page 8; 43pp; English.
XX
XX The invention relates to a synthetic immunogen for inducing specific
XX antibodies against gonadotropin releasing hormone (GnRH) also known as
XX luteinising hormone releasing hormone (LHRH) comprising a fusion peptide
XX which comprises a promiscuous helper T-cell peptide epitope and
XX immunomimic peptide epitope or its analogue. The synthetic immunogen is
XX useful inducing an immune response against GnRH in an animal subject, and
XX as such is useful as a contraceptive and in the treatment of diseases
XX such as cancer (of the breast, uterus and other gynaecological cancer),
XX endometriosis, uterine fibroids, benign prostatic hypertrophy and
XX prostate cancer. The immunogen is effective in eliciting high and
XX specific anti-GnRH antibody titres. The present sequence is a synthetic
XX immunogen of the invention
XX
XX Sequence 33 AA;
XX
XX Query Match 55.1%; Score 81.5; DB 5; Length 33;
XX Best Local Similarity 66.7%; Pred. No. 3.4e-05;
XX Matches 16; Conservative 2; Mismatches 5; Indels 1; Gaps 1;
XX
XX Qy 4 KANSKFIGITELGPSLHWSYGLRP 27
XX ||||| : ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX Db 10 KASSVF-NVANSGPSLHWSYGLRP 32
XX ||||| : ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX
XX RESULT 15
XX AAO30489
XX ID AAO30489 standard; protein; 194 AA.
XX
XX AC AAO30489;
XX
XX 22-SEP-2003 (first entry)
XX
XX Human TNFalpha variant, TNF34-P30-P2.
XX
XX Multimeric protein; interleukin 5; IL5; TNFalpha; inflammatory disease;
XX tumour necrosis factor alpha; gene therapy; arthritis; human; mutant;
XX mutein; variant; tetanus toxoid; epitope.
XX
XX Homo sapiens.
XX Unidentified.
XX
OS

```

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OS Chimeric.
XX Key Location/Qualifiers
FH Region 1. .109
FT Region /note= "Human TNF"
FT Region 110. .130
FT Region /note= "Tetanus toxoid P30 epitope"
FT Region 131. .145
FT Region /note= "Tetanus toxoid P2 epitope"
FT Region 146. .194
FT Region /note= "Human TNF"
XX WO2003042244-A2.
XX
XX 22-MAY-2003.
XX
XX 15-NOV-2002; 2002WO-DK000764.
XX
XX 16-NOV-2001; 2001DX-00001702.
XX
XX 16-NOV-2001; 2001US-0331575P.
XX
XX (PHAR-) PHARMEXA AS.
XX (KLYS/) KLYSNER S.
XX (NIEL/) NIELSEN F S.
XX (BRAT/) BRATT T.
XX (VOLD/) VOLDBOG B.
XX (MOUR/) MOURITSEN S.
XX
XX Klysner S, Nielsen FS, Bratt T, Voldborg B, Mouritsen S;
XX WPI; 2003-449558/42.
XX
XX PT New immunogenic analogue of a polymeric protein, useful for preparing a
XX composition for treating inflammatory diseases e.g. arthritis.
XX Claim 23; Page 159-160; 196pp; English.
XX
XX The invention relates to immunogenic analogues of multimeric proteins
XX such as immunogenic variants of interleukin 5 (IL5) and tumour necrosis
XX factor alpha (TNF, TNFalpha) and methods for production of immunogenic
XX analogues. The immunogenic analogue is useful for preparing a composition
XX for treating inflammatory diseases, e.g., arthritis. It is also used in
XX gene therapy. The present sequence is human TNFalpha variant protein with
XX an inserted tetanus toxoid P2 and P30 epitopes. This sequence is used to
XX illustrate the method of the invention
XX
XX Sequence 194 AA;
XX
XX Query Match 54.7%; Score 81; DB 6; Length 194;
XX Best Local Similarity 76.2%; Pred. No. 0.0003;
XX Matches 16; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
XX
XX QY 1 QYIKANSKFIGITELQPSLHW 21
XX
XX Db 131 QYIKANSKFIGITELAEAKPW 151
XX
XX Search completed: March 10, 2004, 09:12:10
XX Job time : 42.1634 secs

```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 10, 2004, 08:58:54 ; Search time 27.6732 Seconds
(without alignments)
319.245 Million cell updates/sec

Title: US-09-848-834a-11

Perfect score: 148

Sequence: 1 QVINKSKFIGHTELGSLHWSYGLRPX 28

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_25.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_virus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	ID	Description
1	74	50.0	1310 2 Q93N27	Q93N27 clostridium
2	53	35.8	751 16 Q8EFL	Q8EFL pseudomonas
3	52.5	35.5	342 16 Q8FZO	Q8FZO thizobium l
4	52	35.1	91 13 Q8PRH0	Q8PRH0 arguilla ja
5	52	35.1	226 12 Q8BAZ8	Q8BAZ8 hepatitis b
6	52	35.1	382 5 Q95VY3	Q95VY3 lumbricus t
7	51.5	34.8	834 16 Q8U7P1	Q8U7P1 agrobacteri
8	51	34.5	384 5 Q77072	O77072 eisenia foe
9	51	34.5	388 17 Q9YD14	Q9YD14 aeropyrum p
10	51	34.5	524 4 Q8N8Z6	Q8N8Z6 homo sapien
11	51	34.5	539 4 Q81YK5	Q81YK5 homo sapien
12	50.5	34.1	60 7 Q31585	Q31585 salmo salar
13	50.5	34.1	71 7 Q9XBJ9	Q9XBJ9 salvelinus
14	50.5	34.1	85 7 Q95IS2	Q95IS2 salmo salar
15	50.5	34.1	85 7 Q95HY1	Q95HY1 salmo salar
16	50.5	34.1	86 7 Q95HX4	Q95HX4 salmo salar

17	50.5	34.1	244	7	Q31590	Q31590 salmo salar
18	50	33.8	94	13	Q8UUK6	Q8UUK6 scleropages
19	50	33.8	274	3	O14264	O14264 schizosacch
20	50	33.8	344	16	Q89RX8	Q89RX8 bradyrhizob
21	50	33.8	480	16	Q91482	Q91482 pseudomonas
22	49.5	33.4	67	7	Q31578	Q31578 salmo salar
23	49	33.1	103	12	Q8QSV9	Q8QSV9 hepatitis b
24	49	33.1	324	12	Q89Y14	Q89Y14 sonchus vel
25	49	33.1	484	16	Q8HZ30	Q8HZ30 pseudomonas
26	48	32.4	226	12	Q71672	Q71672 hepatitis b
27	48	32.4	232	16	Q888R4	Q888R4 pseudomonas
28	48	32.4	318	16	Q8UE59	Q8UE59 agrobacteri
29	48	32.4	334	16	Q89Y42	Q89Y42 bradyrhizob
30	48	32.4	794	16	Q82DY5	Q82DY5 versinia pe
31	48	32.4	1036	16	Q8PIX2	Q8PIX2 xanthomonas
32	48	32.4	2091	3	P78616	P78616 emericella
33	47.5	32.1	84	13	Q9DEK4	Q9DEK4 coregonus s
34	47.5	32.1	85	7	Q95IS3	Q95IS3 salmo salar
35	47.5	32.1	85	7	Q95IR2	Q95IR2 salmo salar
36	47.5	32.1	149	7	Q31495	Q31495 oncorhynch
37	47.5	32.1	205	17	Q981D4	Q981D4 sulfolobus
38	47.5	32.1	216	7	Q9GJH0	Q9GJH0 salmo trutt
39	47.5	32.1	216	7	Q9GJG9	Q9GJG9 salmo trutt
40	47.5	32.1	1361	12	Q8BF56	Q8BF56 tulip virus
41	47	31.8	114	10	Q8L8X1	Q8L8X1 arabidopsis
42	47	31.8	134	10	Q9LSN9	Q9LSN9 arabidopsis
43	47	31.8	230	8	Q8HMC7	Q8HMC7 physcillus
44	47	31.8	323	10	Q7Y0Z6	Q7Y0Z6 lycopersico
45	47	31.8	342	16	Q82TX0	Q82TX0 nitrosomona

ALIGNMENTS

RESULT 1
Q93N27 PRELIMINARY; PRT; 1310 AA.
ID Q93N27 AC Q93N27; 2001 (TREMREL. 19, Created)
DT 01-DEC-2001 (TREMREL. 19, Last sequence update)
DT 01-OCT-2003 (TREMREL. 25, Last annotation update)
DE Tetanus toxin (Fragment).
OS Clostridium tetani.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium
OX NCBI_TaxID=1513;
RN [1]
RP SEQUENCE FROM N.A.
RA Shumin Z., Dianliang L.;
RT "Cloning and sequence analysis of tetanus toxin gene."
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF389424; AK72964.2; ...
DR GO: 0004866; F: endopeptidase inhibitor activity; IEA.
DR GO: 0008237; F: metalloproteinase activity; IEA.
DR GO: 0015070; F: zinc ion binding; IEA.
DR GO: 0008270; F: zinc ion binding; IEA.
DR GO: 0009405; P: pathogenesis; IEA.
DR GO: 0006508; P: proteolysis and peptidolysis; IEA.
DR InterPro: IPR008985; ConA like lec_g1.
DR InterPro: IPR001064; Crystallin.
DR InterPro: IPR002160; Kunitz legume.
DR InterPro: IPR000395; Peptidase M27.
DR InterPro: IPR006025; Pept M27.
DR Pfam: PF01742; Peptidase M27; I.
DR PRINTS: PR00760; BONTOXILYSIN.
DR ProDom: PD001963; Bontoxilysin; 1.
DR PROSITE: PS00225; CRYSTALLIN_BETAGAMMA; 1.
FT NON TER 1 1310
SQ SEQUENCE 1310 AA; 150316 MW; 9EADDC914418E450 CRC64;
Query Match 50.0%; Score 74; DB 2; Length 1310;

Best Local Similarity 100.0%; Pred. No. 0.023; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QYKANSKFIGITEL 15
 |||||
 Db 831 QYKANSKFIGITEL 845

RESULT 2

ID Q88EF1 PRELIMINARY; PRT; 751 AA.
 AC Q88EF1
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Conserved hypothetical protein.
 GN PP4514
 OS Pseudomonas putida (strain KT2440).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=150488;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22423060; PubMed=12534463;

RA Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
 RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
 RA Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J.,
 RA Madupu R., Nelson W., White O., Peterson J., Khouri H., Hance I.,
 RA Chris Lee P., Holtzapfle E., Scanlan D., Tran K., Moazzes A.,
 RA Uterback T., Rizzo M., Lee K., Kosack D., Moestl D., Wedler H.,
 RA Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.,
 RA Krawitz C., Eissen J., Timmis K.N., Duesterhoeft A., Tuemmier B.,
 RA Fraser C.M.;
 RT "Complete genome sequence and comparative analysis of the
 RT metabolically versatile Pseudomonas putida KT2440."
 RL Environ. Microbiol. 4:799-808(2002).
 DR EMBL; AE016790; AAN70088.1; -;
 DR TIGR; PP4514; -;
 DR GO; GO:0003824; F:catalytic activity; IEA.
 DR GO; GO:0045735; P:nutrient reservoir activity; IEA.
 DR InterPro; IPR002641; Patatin.
 DR Pfam; PF01734; Patatin; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 751 AA; 83174 MW; CD140194E4CA6368 CRC64;

Query Match 35.8%; Score 53; DB 16; Length 751;
 Best Local Similarity 58.3%; Pred. No. 23;
 Matches 14; Conservative 4; Mismatches 4; Indels 2; Gaps 2;

Qy 2 YKANSKFIGI-TELGP-SLHWSYG 24
 |||||
 Db 712 YKANSKFIGI-TELGP-SLHWSYG 734

RESULT 3

ID Q98FZ0 PRELIMINARY; PRT; 342 AA.
 AC Q98FZ0
 DT 01-OCT-2001 (TREMBlrel. 18, Created)
 DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Hypothetical protein ml13560.
 GN ML13560.
 OS Rhizobium loti (Mesorhizobium loti).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Phyllobacteriaceae; Mesorhizobium.
 OX NCBI_TaxID=381;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MAFF303099;
 RX MEDLINE=21082930; PubMed=11214968;
 RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
 RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,

RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsumo A.,
 RA Mochizuki Y., Nakayama S., Nakazaki N., Shimo S., Sugimoto M.,
 RA Takeuchi C., Yamada M., Tabata S.;
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
 RT Mesorhizobium loti";
 RL DNA Res. 7:331-338(2000).
 DR EMBL; AP003002; BAB50426.1; -;
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 342 AA; 37582 MW; 99597D57D25D11A1 CRC64;

Query Match 35.5%; Score 52.5; DB 16; Length 342;
 Best Local Similarity 37.5%; Pred. No. 11;
 Matches 9; Conservative 7; Mismatches 5; Indels 3; Gaps 1;

Qy 1 QYKANSKFIGITELGP-SLHWSYG 24
 |||||
 Db 82 RFLKAGSDFIGVADTG--YWFPG 102

RESULT 4

ID Q9PRH0 PRELIMINARY; PRT; 91 AA.
 AC Q9PRH0
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Prepro-mGnRH precursor (Gonadoliberin) (Gonadotropin-releasing
 hormone) (LH-RH) (Luliberin).
 OS Anguilla japonica (Japanese eel).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;
 OC Anguilla.
 OX NCBI_TaxID=7937;
 RN [1]_TaxID=7937;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Okubo K., Suetake H., Aida K.;
 RT "Expression of two gonadotropin-releasing hormone (GnRH) precursor
 RT genes in various tissues of the Japanese eel and evolution of GnRH.";
 RL Zool. Sci. 16:471-478(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Okubo K., Suetake H., Aida K.;
 RT "A splicing variant for the prepro-mammalian gonadotropin-releasing
 RT hormone (prepro-mGnRH) mRNA is present in the brain and various
 RT peripheral tissues of the Japanese eel.";
 RL Zool. Sci. 16:645-651(1999).
 CC -!- FUNCTION: STIMULATES THE SECRETION OF GONADOTROPINS (BY
 CC SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE GnRH FAMILY.
 DR EMBL; AB026989; BAB82608.1; -;
 DR EMBL; AB026991; BAB83597.1; -;
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005183; F:luteinizing hormone-releasing factor activity; IEA.
 DR GO; GO:0007275; P:development; IEA.
 DR InterPro; IPR002012; GnRH.
 DR InterPro; IPR004079; Gonadoliberin1.
 DR Pfam; PF00446; GnRH; 1.
 DR PRINTS; PR01541; GONADOLIBERN1.
 DR PROSITE; PS00473; GnRH; 1.
 KW Amidation; Hormone; Signal.
 FT SIGNAL 1 22 POTENTIAL.
 FT CHAIN 23 32 MGNRH.
 FT CHAIN 33 91 GnRH ASSOCIATED PEPTIDE.
 SQ SEQUENCE 91 AA; 9893 MW; BA15C9DC08434A7B CRC64;

Query Match 35.1%; Score 52; DB 13; Length 91;
 Best Local Similarity 100.0%; Pred. No. 2.9;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 20 HWSYGLRP 27
 |||||
 Db 24 HWSYGLRP 31

```

RESULT 5
Q8BAZ8      PRELIMINARY;      PRT;      226 AA.
ID Q8BAZ8;
AC Q8BAZ8;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Surface antigen.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=P078;
RA Bowden R.J.;
RT "Hepatitis B virus variability and human population history in the Pacific.";
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=P078;
RA Basuni A.A., Bowden R.J., Butterworth L.-A., Cooksley G., Locarnini S., Carman W.F.;
RL EMBL; AX124488; AAM82819.1; -.
DR GO; GO:0016032; Pivital life cycle; IEA.
DR InterPro; IPR000349; Hepvir_surfac.
DR Pfam; PF00695; VMSA; 1.
SQ SEQUENCE 226 AA; 25414 MW; 63791C8AEFFB514 CRC64;

Query Match      35.1%; Score 52; DB 12; Length 226;
Best Local Similarity 39.1%; Pred. No. 8.2;
Matches 9; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

RESULT 6
Q95VY3      PRELIMINARY;      PRT;      382 AA.
ID Q95VY3;
AC Q95VY3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Coelomic cytolytic factor precursor.
OS Lumbriacus terrestris (Common earthworm).
OC Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida; Lumbricina; Lumbricidae; Lumbricus.
OX NCBI_TaxID=6398;
RN [1]
RP SEQUENCE FROM N.A.
RA Beschlin A., De Baetselier P., Bilej M.;
RT "Distinct carbohydrate recognition domains of an earthworm defense molecule recognize Gram negative and Gram positive bacteria.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF395805; AAL09587.1; -.
DR GO; GO:0004553; Phylolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0005975; P-carbohydrate metabolism; IEA.
DR InterPro; IPR008985; ConA like lec.gl.
DR Pfam; PF00722; Glyco_hydro_16; 1.
DR Signal.
FT SIGNAL
SQ SEQUENCE 382 AA; 43931 MW; 5256CF171EB7D3FB CRC64;

Query Match      35.1%; Score 52; DB 5; Length 382;
Best Local Similarity 36.8%; Pred. No. 15;
Matches 7; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

RESULT 7
Q8U7P1      PRELIMINARY;      PRT;      834 AA.
ID Q8U7P1;
AC Q8U7P1;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Periplasmic nitrate reductase large subunit.
GN NAPA OR ATU4408 OR AGR L 917.
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
OX NCBI_TaxID=176299;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608550; PubMed=11743193;
RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P., Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L., Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr., Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C., Kutyavin I., Levy R., Li M.-J., McClelland E., Palmeri A., Gordon D., Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D., Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M., Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M., Chumley P., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V., Nester E.W.;
RA "The genome of the natural genetic engineer Agrobacterium tumefaciens C58.";
RL Science 294:2317-2323 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608551; PubMed=11743194;
RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L., Roumel K., Gordon J., Vaudin M., Lartchouk O., Epp A., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B., Flanagan C., Crowell C., Gursen J., Lomo C., Sear C., Strub G., Cielo C., Slater S.;
RA "Genome sequence of the plant pathogen and biotechnology agent Agrobacterium tumefaciens C58.";
RL Science 294:2323-2328 (2001).
DR EMBL; AB009369; AAL45202.1; ALT_INIT.
DR EMBL; AE008245; AAK89031.1; -.
DR PIR; AD3098; AD3098.
DR PIR; E98188; E98188.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR009010; Asp decarb fold.
DR InterPro; IPR006656; Molybdopterin.
DR InterPro; IPR006963; Molybdop_Fe4S4.
DR InterPro; IPR006657; Mol_dinuc_bind.
DR InterPro; IPR006655; Prok_Mboxred.
DR InterPro; IPR006311; Tat.
DR Pfam; PF0384; molybdopterin; 1.
DR Pfam; PF04879; Molybdop_Fe4S4; 1.
DR Pfam; PF01568; Molybdop binding; 1.
DR TIGRfam; TIGR01409; TAT signal seq; 1.
DR PROSITE; PS00551; MOLYBDOPTERIN_PROK_1; 1.
DR Complete proteome.
SQ SEQUENCE 834 AA; 93527 MW; FF707BC71CA08B9E CRC64;

Query Match      34.8%; Score 51.5; DB 16; Length 834;
Best Local Similarity 37.0%; Pred. No. 44;
Matches 10; Conservative 9; Mismatches 1; Indels 7; Gaps 2;

QY 2 YIKANSKFI-GITELGSLHWSYGLRP 27
Db 289 FVRNHTKFGVGTDIG-----YGLRP 309
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RESULT 8
O77072 ID O77072 PRELIMINARY; PRT; 384 AA.
AC O77072;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Coelomic cytolitic factor 1.
GN CCFL.
OS Eiseinia foetida (Common branding worm) (Common dung-worm).
OC Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
OC Lumbricina; Lumbricidae; Eiseinia.
OX NCBI_TaxID=6396;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98406152; PubMed=9733802;
RA Beschin A., Bilek M., Hanssens F., Raymakers J., Van Dyck E.,
RA Revett H., Brys L., Gomez J., De Baetselier P., Timmermans M.;
RT "Identification and cloning of a glucan- and Lipopolysaccharide-
RT binding protein from Eiseinia foetida earthworm involved in the
RT activation of prophenoloxidase cascade.";
RL J. Biol. Chem. 273:24948-24954 (1998).
DR EMBL; AF030028; AAC35889.1; -.
DR GO; GO:0004553; F:Hydrolase activity, hydrolyzing O-glycosyl . . . ; IEA.
DR GO; GO:0005975; P:Carbohydrate metabolism; IEA.
DR InterPro; IPR008985; ConsA-like lec gl.
DR InterPro; IPR000757; Glyco_hydro.16.
DR Pfam; PF00722; Glyco_hydro.16; 1.
SQ SEQUENCE 384 AA; 44322 MW; C90B5C94003BAD6D CRC64;

Query Match 34.5%; Score 51; DB 5; Length 384;
Best Local Similarity 41.2%; Pred. No. 22;
Matches 7; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

OY 8 KPFGITELGPSLHWSYG 24
..:..:..:..:..:..:
DB 198 EPLGIQKMGSTWHNPG 214

RESULT 9
O9YD14 ID O9YD14 PRELIMINARY; PRT; 388 AA.
AC O9YD14;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 388AA long hypothetical FMU protein.
GN APEI098.
OS Aeropyrum pernix.
OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
OC Desulfurococceae; Aeropyrum.
OX NCBI_TaxID=56636;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=K1;
RX MEDLINE=99310339; PubMed=10382966;
RA Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H.,
RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
RA Yamazaki J., Kishida N., Oguchi A., Aoki K.-I., Kubota K.,
RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
RT "Complete genome sequence of an aerobic hyper-thermophilic
RT crenarchaeon, Aeropyrum pernix K1.";
RL DNA Res. 6:83-101 (1999).
DR EMBL; AP000060; BAA80083.1; -.
DR PIR; C72710; C72710.
DR GO; GO:0003723; F:RNA binding; IEA.
DR InterPro; IPR002478; PUA.
DR InterPro; IPR001678; Sun_Nop1/Nop2.
DR InterPro; IPR004521; Unchar_dom.2.
DR Pfam; PF01189; Noll_Nop2_Sun; 1.

Pfam; PF01472; PUA; 1.
SMART; SM00359; PUA; 1.
DR TIGRFAMs; TIGR00451; unchar_dom_2; 1.
DR PROSITE; PS00890; PUA; 1.
KW Complete proteome.
SQ SEQUENCE 388 AA; 42535 MW; A9E10CEAAAEF0B0AC CRC64;

Query Match 34.5%; Score 51; DB 17; Length 388;
Best Local Similarity 71.4%; Pred. No. 22;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 14 ELGPSLHWSYGLRP 27
||| ||| ||| |||
DB 345 ELGRLTWSWGLRP 358

RESULT 10
Q8N826 ID Q8N826 PRELIMINARY; PRT; 524 AA.
AC Q8N826;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein FLJ38654.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Nishi T., Ota T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H.,
RA Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S.,
RA Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
RA Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M.,
RA Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Kanehori K.,
RA Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y.,
RA Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
RT "NEDO human cDNA sequencing project."
RT Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RL -!- SIMILARITY: CONTAINS 1 CUB DOMAIN.
CC EMBL; AK095973; BAC04663.1; -.
DR GO; GO:0007155; P:Cell adhesion; IEA.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000421; FA58 C.
DR InterPro; IPR008979; Gal_Bind-like.
DR InterPro; IPR004043; LCCL_dom.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00754; F5_F8_type_C; 1.
DR Pfam; PF03815; LCCL; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00231; FA58C; 1.
DR SMART; SM00603; LCCL; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS00022; FA58C_3; 1.
DR PROSITE; PS00820; LCCL; 1.
KW Hypothetical protein.
SQ SEQUENCE 524 AA; 57698 MW; CEAC4F78A492EB44 CRC64;

Query Match 34.5%; Score 51; DB 4; Length 524;
Best Local Similarity 40.9%; Pred. No. 31;
Matches 9; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

OY 3 IKANSKFITELGPSLHWSYG 24
||| : : : :
DB 267 IRASSSQVNSGQDVHSPG 288

RESULT 11
Q81YK5 ID Q81YK5 PRELIMINARY; PRT; 539 AA.
AC Q81YK5
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
Pfam; PF01189; Noll_Nop2_Sun; 1.
```

DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
 DE Similar to RIKEN cDNA 4631413K11 gene.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC035671; AAH35671.1; -.
 DR Genew; HGNC:21479; DBLDD1.
 DR GO; GO:0007155; P:cell adhesion; IEA.
 DR InterPro; IPR000859; CUB.
 DR InterPro; IPR000421; FAS8.C.
 DR InterPro; IPR008979; Gal bind like.
 DR InterPro; IPR004043; LCCL_dom.
 DR Pfam; PF00431; CUB; 1.
 DR Pfam; PF00754; F5_P8_type_C; 1.
 DR Pfam; PF03815; LCCL; 1.
 DR SMART; SM00042; CUB; 1.
 DR SMART; SM00231; FAS8C; 1.
 DR SMART; SM00603; LCCL; 1.
 DR PROSITE; PS01180; CUB; 1.
 DR PROSITE; PS00022; FAS8C.3; 1.
 DR PROSITE; PS00820; LCCL; 1.
 SQ SEQUENCE 539 AA; 59196 MW; 929D4BIACIAAAA4C CRC64;

 Query Match 34.5%; Score 51; DB 4; Length 539;
 Best Local Similarity 40.9%; Pred. No. 32;
 Matches 9; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

 QY 3 IKANSKFIGITELGPSLWSYG 24
 Db 267 IRASSWSQVNSGGQVHWSPG 288

 RESULT 12
 Q31585
 ID Q31585 PRELIMINARY; PRT; 60 AA.
 AC Q31585;
 DT 01-NOV-1996 (TEMBLrel. 01, Created)
 DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
 DE (DB02) MHC class II beta 1 (Fragment).
 OS Salmo salar (Atlantic salmon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
 OX NCBI_TaxID=8030;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Gimholt U., Oleaker I., de Vries Lindstrom C., Lie O.;
 RA "A study of polymorphism in the MHC class II beta 1 and MHC class I
 RT alpha 2 domain exons of Atlantic salmon (Salmo salar).";
 RL Submitted (OCT-1993) to the EMBL/GenBank/DBJ databases.
 DR EMBL; L24953; AAA49597.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0045012; F:MHC class II receptor activity; IEA.
 DR GO; GO:0019844; P:antigen presentation, exogenous antigen; IEA.
 DR GO; GO:0019886; P:antigen processing, exogenous antigen via M...; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR000353; MHC_II_beta.
 DR Pfam; PF00969; MHC_II_beta; 1.
 DR ProDom; PD000328; MHC_II_beta; 1.
 KW Glycoprotein; MHC II; Transmembrane.
 FT NON_TER 1
 FT NON_TER 60
 SQ SEQUENCE 60 AA; 6776 MW; 5DAF3449060940E2 CRC64;

 Query Match 34.1%; Score 50.5; DB 7; Length 60;
 Best Local Similarity 57.9%; Pred. No. 3.1;

Matches 11; Conservative 3; Mismatches 2; Indels 3; Gaps 1;

 QY 1 QYIKANS---KFIGITELG 16
 Db 16 EYIRFNSVGVGVGYTELG 34

 RESULT 13
 Q9XRJ9
 ID Q9XRJ9 PRELIMINARY; PRT; 71 AA.
 AC Q9XRJ9;
 DT 01-NOV-1999 (TEMBLrel. 12, Created)
 DT 01-NOV-1999 (TEMBLrel. 12, Last sequence update)
 DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
 DE MHC class II beta 1 (Fragment).
 OS SANA.
 OS Salvelinus namaycush (lake trout).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Salvelinus.
 OX NCBI_TaxID=8040;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Dorschner M.O., Duris T., Phillips R.B.;
 RA "Diversity of a Lake Trout Mhc class II Gene";
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF130026; AAD20889.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0045012; F:MHC class II receptor activity; IEA.
 DR GO; GO:0019884; P:antigen presentation, exogenous antigen; IEA.
 DR GO; GO:0019886; P:antigen processing, exogenous antigen via M...; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR000353; MHC_II_beta.
 DR Pfam; PF00969; MHC_II_beta; 1.
 DR ProDom; PD000328; MHC_II_beta; 1.
 KW Glycoprotein; MHC II; Transmembrane.
 FT NON_TER 1
 FT NON_TER 71
 SQ SEQUENCE 71 AA; 8002 MW; E3095286582A9F2D CRC64;

 Query Match 34.1%; Score 50.5; DB 7; Length 71;
 Best Local Similarity 57.9%; Pred. No. 3.7;
 Matches 11; Conservative 3; Mismatches 2; Indels 3; Gaps 1;

 QY 1 QYIKANS---KFIGITELG 16
 Db 14 EYIRFNSVGVGVGYTELG 32

 RESULT 14
 Q95IS2
 ID Q95IS2 PRELIMINARY; PRT; 85 AA.
 AC Q95IS2;
 DT 01-DEC-2001 (TEMBLrel. 19, Created)
 DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
 DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
 DE MHC class II beta chain (Fragment).
 OS Salmo salar (Atlantic salmon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
 OX NCBI_TaxID=8030;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Landry C., Bernatchez L.;
 RA "Comparative analysis of population structure across environments and
 RT geographic scales at Major Histocompatibility Complex and
 RT microsatellite in Atlantic salmon (Salmo salar).";
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF373699; AAK51882.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0045012; F:MHC class II receptor activity; IEA.
 DR GO; GO:0019884; P:antigen presentation, exogenous antigen; IEA.

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OM protein - protein search, using sw model

Run on: March 10, 2004, 08:58:54 ; Search time 8.71595 Seconds
(without alignments)
309.015 Million cell updates/sec

Title: US-09-848-834A-11

Perfect score: 148

Sequence: 1 QYIKANSKFIGITELGPSLHWSYGLRPX 28

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*

1: piri: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	74	50.0	1315	1 BTCLTN	tentoxilysin (EC 3
2	54	36.5	67	2 I78541	gonadoliberin prec
3	54	36.5	90	1 RHMSG	gonadoliberin prec
4	54	36.5	92	1 RHUG	gonadoliberin prec
5	54	36.5	92	1 RHRTG	gonadoliberin prec
6	52	35.1	10	1 RHPOG	gonadoliberin - pi
7	52	35.1	10	1 RHSHG	gonadoliberin - sh
8	52	35.1	89	2 I51423	gonadoliberin prec
9	51.5	34.8	824	2 AD3098	periplasmic nitrat
10	51.5	34.8	834	2 E98188	probable fmu prote
11	51	34.5	388	2 C72710	class II histocomp
12	50.5	34.1	244	2 S29982	hypothetical prote
13	50	33.8	274	2 T39087	probable MPS trans
14	50	33.8	480	2 A83487	hypothetical prote
15	49	33.1	422	2 T39662	potassium uptake p
16	49	33.1	484	2 E83245	hemocytin - silkw
17	49	33.1	3133	2 S52093	gonadoliberin i -
18	48	32.4	10	1 RHAQ1	gonadoliberin i pr
19	48	32.4	92	2 I50644	transketolase [imp
20	48	32.4	318	2 AD2810	probable transket
21	48	32.4	318	2 G97588	pyruvate, water di
22	48	32.4	794	2 AB0294	conserved hypothet
23	47.5	32.1	205	2 C90140	hypothetical prote
24	47	31.8	728	2 E83228	hypothetical prote
25	46.5	31.4	193	2 F89967	class II histocomp
26	46.5	31.4	245	2 S29980	hypothetical prote
27	46.5	31.4	388	2 A82445	gonadotropin-relea
28	46	31.1	98	2 I50739	hypothetical prote
29	46	31.1	171	2 S38237	

30	46	31.1	186	2 A90167	adenylate cyclase,
31	46	31.1	349	2 E75611	glucosamine-fructo
32	46	31.1	459	2 G82431	C4-dicarboxylate t
33	46	31.1	522	2 T43369	pyruvate, water di
34	46	31.1	780	2 D75361	phosphoenolpyruvat
35	46	31.1	4056	2 H96599	protein F14J6.10
36	45.5	30.7	322	2 T98399	probable amidohydr
37	45	30.4	256	2 T50616	hypothetical prote
38	45	30.4	258	2 F72052	peptidyl-prolyl ci
39	45	30.4	258	2 B85773	FKBP-type peptidyl
40	45	30.4	368	2 T27432	hypothetical prote
41	45	30.4	397	2 B70815	probable transamin
42	45	30.4	435	2 C89857	conserved hypothet
43	45	30.4	456	2 S55661	hypothetical prote
44	45	30.4	644	2 S46746	hypothetical prote
45	45	30.4	674	2 H72423	alpha-glucuronidas

ALIGNMENTS

RESULT 1

BTCLTN
tentoxilysin (EC 3.4.24.68) precursor - Clostridium tetani
N/Alternate names: tetanus neurotoxin
C/Species: Clostridium tetani
C/Date: 31-Mar-1988 #sequence_revision 31-Mar-1989 #text change 03-Jun-2002
C/Accession: A25689; A25757; A25194; B25194; A60759; S63348; S89364
R/Eisel, U.; Jarasch, W.; Goretzki, K.; Henschen, A.; Engels, J.; Weller, U.; Hudel,
EMBO J. 5, 2495-2502, 1986
A/Title: Tetanus toxin: primary structure, expression in E. coli, and homology with bc
A/Reference number: A25689; MUID:87053814; PMID:3536478
A/Accession: A25689
A/Molecule type: DNA
A/Residues: 1-1315 <EIS>
A/Cross-references: GB:X04436; NID:G40769; PIDN:CAA28033.1; PID:G40770
R/Fairweather, N.F.; Lyness, V.A.
Nucleic Acids Res. 14, 7809-7812, 1986
A/Title: The complete nucleotide sequence of tetanus toxin.
A/Reference number: A25757; MUID:87040747; PMID:3774547
A/Accession: A25757
A/Molecule type: DNA
A/Residues: 1-1315 <FAI>
A/Cross-references: GB:X06214; NID:G40773; PIDN:CAA29564.1; PID:G40774
R/Fairweather, N.F.; Lyness, V.A.; Pickard, D.J.; Allen, G.; Thomson, R.O.
J. Bacteriol. 165, 21-27, 1986
A/Title: Cloning, nucleotide sequencing, and expression of tetanus toxin fragment C in
A/Reference number: A25194; MUID:86085672; PMID:3510187
A/Accession: A25194
A/Molecule type: DNA
A/Residues: 743-1315 <FA2>
A/Cross-references: GB:M12739; NID:G144920; PIDN:AAA23282.1; PID:G144921
A/Accession: B25194
A/Molecule type: protein
A/Residues: 865-894 <PAJ>
R/Matsuda, M.; Lei, D.L.; Sugimoto, N.; Ozutsuni, K.; Okabe, T.
Infect. Immun. 57, 3588-3593, 1989
A/Title: Isolation, purification, and characterization of fragment B, the NH-2-termina
A/Reference number: A60759; MUID:90035436; PMID:2478476
A/Accession: A60759
A/Molecule type: Protein
A/Residues: 461-475 <NAR>
R/Demotz, S.; Lanzavecchia, L.; Eisel, U.; Niemann, H.; Widmann, C.; Corradin, G.
J. Immunol. 142, 394-402, 1989
A/Title: Delineation of several DR-restricted tetanus toxin T cell epitopes.
A/Reference number: J50098; MUID:89093918; PMID:2463305
A/Contents: annotation; epitope region
R/Schiavo, G.; Benfenati, F.; Poulain, B.; Rossetto, O.; de Laureto, P.P.; DasGupta, B
Nature 359, 832-835, 1992
A/Title: Tetanus and botulinum-B neurotoxins block neurotransmitter release by proteol
A/Reference number: S27125; MUID:93063293; PMID:1331807
A/Contents: annotation

R;de Filippis, V.; Vangelista, L.; Schiavo, G.; Tonello, F.; Montecucco, C.
 Eur. J. Biochem. 229, 61-69, 1995
 A;Title: Structural studies on the zinc-endoropeptidase light chain of tetanus neurotoxin.
 A;Reference number: S69348; MUID:95262688; PMID:7744050
 A;Accession: S69348
 A;Molecule type: protein
 A;Residues: 2-31 <DEF>
 C;Comment: The source of this protein was an extrachromosomal plasmid.
 C;Comment: The precursor is cleaved by endogenous proteinase activity to form light (fra
 dual chains are not toxic when separated). The amino end of the heavy chain (fragment B)
 C;Comment: Fragment B forms ion channels in a lipid bilayer. Fragment C binds to gangli
 C;Comment: This potent neurotoxin binds to peripheral neuronal synapses, is internalized
 presynaptic neurons. It inhibits neurotransmitter release by proteolytic cleavage of sy
 C;Function:
 A;Description: blocks neuroexcitotoxicity via hydrolysis of a Gln-Phe peptide bond in synap
 C;Superfamily: tetanus toxin
 C;Keywords: hydrolase; metalloproteinase; neurotoxin; transmembrane protein; zinc
 F;2-457/Product: tetroxylsine light chain (fragment A) #status predicted <TTL>
 F;461-1115/Product: tetroxylsine heavy chain (fragment B.C) #status experimental <TTH>
 F;461-864/Domain: channel forming (fragment B) #status predicted <TXB>
 F;865-1315/Domain: ganglioside binding (fragment C) #status predicted <TXC>
 F;233,237/Binding site: zinc (His) #status predicted
 F;234/Active site: Glu #status predicted

Query Match 50.0%; Score 74; DB 1; Length 1315;
 Best Local Similarity 100.0%; Pred. No. 0.021;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYIKANSKFIGITEL 15
 DB 830 QYIKANSKFIGITEL 844

RESULT 2

178541
 Gonadoliberin precursor - rhesus macaque (fragment)
 N;Alternate names: luteinizing hormone releasing hormone
 C;Species: Macaca mulatta (rhesus macaque)
 C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 16-Jul-1999
 C;Accession: I78541
 R;Ma, Y.J.; Costa, M.E.; Ojeda, S.R.
 Neuroendocrinology 60, 346-359, 1994
 A;Title: Developmental expression of the genes encoding transforming growth factor alpha
 A;Reference number: 158134; MUID:95124501; PMID:7545971
 A;Accession: I78541
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-67 <RES>
 A;Cross-references: GB:S75918; NID:g912831; PIDN:AA833096.1; PID:g912832
 C;Superfamily: gonadoliberin

Query Match 36.5%; Score 54; DB 2; Length 67;
 Best Local Similarity 90.0%; Pred. No. 0.69;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 18 SLHWSYGLRUP 27
 DB 5 SQHWSYGLRUP 14

RESULT 3

RHWSG
 Gonadoliberin precursor - mouse
 N;Alternate names: gonadotropin-releasing hormone (GNRH); luteinizing hormone releasing
 C;Species: Mus musculus (house mouse)
 C;Date: 31-Dec-1993 #sequence_revision 18-Mar-1997 #text_change 18-Jun-1999
 C;Accession: A47578
 R;Ma, Y.J.; Costa, M.E.; Ojeda, S.R.
 Science 234, 1366-1371, 1986
 A;Title: A deletion truncating the gonadotropin-releasing hormone gene is responsible fo
 A;Reference number: A47578; MUID:87069928; PMID:3024317
 A;Accession: A47578

A;Molecule type: DNA
 A;Residues: 1-90 <MAS>
 A;Cross-references: EMBL:ML4872; NID:g1935576; PIDN:AAA37717.1; PID:g387175
 C;Genetics:
 A;Introns: 45/3; 77/3
 C;Function:
 A;Description: gonadoliberin stimulates pituitary secretion of lutropin and follitropir
 A;Note: gonadoliberin-associated protein may have prolactin release inhibiting activity
 C;Superfamily: gonadoliberin
 C;Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid
 F;1-23/Domain: signal sequence #status predicted <SIG>
 F;1-23/Product: gonadoliberin #status predicted <GLB>
 F;22-31/Product: gonadoliberin-associated protein #status predicted <GAP>
 F;35-90/Product: gonadoliberin-associated protein #status predicted <GLB>
 F;22/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicte
 F;31/Modified site: amidated carboxyl end (Gly) (amide in mature form from following gl

Query Match 36.5%; Score 54; DB 1; Length 90;

Best Local Similarity 90.0%; Pred. No. 0.95;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 18 SLHWSYGLRUP 27
 DB 21 SQHWSYGLRUP 30

RESULT 4

RHUG
 gonadoliberin precursor [validated] - human
 N;Alternate names: gonadotropin releasing hormone (GNRH); luteinizing hormone releasing
 C;Species: Homo sapiens (man)
 C;Date: 17-Mar-1987 #sequence_revision 21-Jul-1995 #text_change 08-Dec-2000
 C;Accession: S05308; A26173; A93342; A90108; A01410; S45718
 R;Hayflick, J.S.; Adelman, J.P.; Seeburg, P.H.
 Nucleic Acids Res. 17, 6403-6404, 1989
 A;Title: The complete nucleotide sequence of the human gonadotropin-releasing hormone g
 A;Reference number: S05308; MUID:8936682; PMID:2671939
 A;Accession: S05308
 A;Status: translation not shown
 A;Molecule type: DNA
 A;Residues: 1-92 <HAY>
 A;Cross-references: EMBL:X15215; NID:g31955; PIDN:CAA33285.1; PID:g31956
 R;Adelman, J.P.; Mason, A.J.; Hayflick, J.S.; Seeburg, P.H.
 Proc. Natl. Acad. Sci. U.S.A. 83, 179-183, 1986
 A;Title: Isolation of the gene and hypothalamic cDNA for the common precursor of gonad
 A;Reference number: A94090; MUID:86094338; PMID:2867548
 A;Accession: A26173
 A;Molecule type: mRNA
 A;Residues: 1-92 <ADE>
 A;Cross-references: GB:M12578; NID:g183418; PIDN:AAA35916.1; PID:g386749
 A;Experimental source: hypothalamus
 R;Seeburg, P.H.; Adelman, J.P.
 Nature 311, 666-668, 1984
 A;Title: Characterization of cDNA for precursor of human luteinizing hormone releasing
 A;Reference number: A93342; MUID:85012739; PMID:6090951

A;Accession: A93342
 A;Molecule type: mRNA
 A;Residues: 1-15, 'S', 17-92 <SEE>
 A;Cross-references: GB:X01059; NID:g34356; PIDN:CAA25526.1; PID:g34357
 A;Experimental source: placenta
 R;Tan, L.; Rousseau, P.
 Biochem. Biophys. Res. Commun. 109, 1061-1071, 1982
 A;Title: The chemical identity of the immunoreactive LHRH-like peptide biosynthesized i
 A;Reference number: A90108; MUID:83126573; PMID:6760865

A;Accession: A90108
 A;Molecule type: protein
 A;Residues: 24-33 <FAN>
 A;Experimental source: placental trophoblasts
 R;Leibovitz, D.; Koch, Y.; Pitzer, F.; Fridkin, M.; Dantes, A.; Baumeister, W.; Amsterc
 FEBS Lett. 346, 203-206, 1994
 A;Title: Sequential degradation of the neuropeptide gonadotropin-releasing hormone by t
 A;Reference number: S45718; MUID:94283597; PMID:8013634
 A;Contents: annotation; degradation pathway of synthetic hormone

C:Genetics:
A:Gene: GDB:GNRH; LHRH: GRH
A:Cross-references: GDB:133746; OMIM:227200; OMIM:152760
A:Map position: 8p21-8p11.2
A:Introns: 47/3; 79/3
C:Function:
A:Description: gonadoliberin stimulates pituitary secretion of lutropin and follitropin
A:Note: gonadoliberin-associated protein may have prolactin release inhibiting activity
C:Superfamily: gonadoliberin
C:Keywords: amidated carboxyl end; hormone; hypothalamus; placenta; pyroglutamic acid
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-92/Product: progadoliberin #status predicted <PGN>
F:24-33/Product: gonadoliberin #status experimental <NAT>
F:37-92/Product: gonadoliberin-associated protein #status predicted <GAP>
F:24/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimental
F:33/Modified site: amidated carboxyl end (Gly) (amide in mature form from following gly

Query Match 36.5%; Score 54; DB 1; Length 92;
Best Local Similarity 90.0%; Pred. No. 0.97; 1; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 18 SLHWSYGLRP 27
DB 23 SQHWSYGLRP 32

RESULT 5
RHRG
Gonadoliberin precursor - rat
N:Alternate names: gonadoliberin-associated protein (GAP); gonadotropin releasing hormone
N:Contains: gonadoliberin; prolactin release-inhibiting factor
C:Species: Rattus norvegicus (Norway rat)
C>Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 18-Jun-1999
C:Accession: A40147; B26173; A48410
R:Bond, C.T.; Hayflick, J.S.; Seeburg, P.H.; Adelman, J.P.
Mol. Endocrinol. 3, 1257-1262, 1989
A:Title: The rat gonadotropin-releasing hormone: SH locus: structure and hypothalamic ex
A:Reference number: A40147; MUID:89384561; PMID:2476669
A:Accession: A40147
A:Molecule type: mRNA
A:Residues: 1-92 <BON>
A:Cross-references: GB:M31670; NID:G204447; PIDN:AAA41264.1; PID:G204448
R:Adelman, J.P.; Mason, A.J.; Hayflick, J.S.; Seeburg, P.H.
Proc. Natl. Acad. Sci. U.S.A. 83, 179-183, 1986
A:Title: Isolation of the gene and hypothalamic cDNA for the common precursor of gonadot
A:Reference number: A94090; MUID:86094338; PMID:2867548
A:Accession: B26173
A:Molecule type: mRNA
A:Residues: 1-92 <ADE>
A:Cross-references: GB:M12579; NID:G204445; PIDN:AAA41263.1; PID:G204446
R:Maier, C.C.; Marchetti, B.; LeBoeuf, R.D.; Blalock, J.E.
Cell. Mol. Neurobiol. 12, 447-454, 1992
A:Title: Thymocytes express a mRNA that is identical to hypothalamic luteinizing hormone
A:Accession: A48410
A:Reference number: A48410; MUID:93105480; PMID:1468115
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-92 <NAI>
A:Cross-references: GB:S50870; NID:G262059; PIDN:AB24572.1; PID:G262060
A:Experimental source: thymus
A:Note: sequence extracted from NCBI backbone (NCBIN:121082, NCBI:P:121083)
C:Genetics:
A:Introns: 47/3; 79/3
C:Function:
A:Description: stimulates pituitary secretion of lutropin and follitropin
A:Note: gonadoliberin-associated protein may have prolactin release inhibiting activity
C:Superfamily: gonadoliberin
C:Keywords: amidated carboxyl end; hormone; hypothalamus; placenta; pyroglutamic acid; r
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-92/Product: progadoliberin #status predicted <PGN>
F:24-33/Product: gonadoliberin #status predicted <Gln>
F:37-92/Product: prolactin release-inhibiting factor #status predicted <PIF>
F:24/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted

F:33/Modified site: amidated carboxyl end (Gly) (amide in mature form from following g

Query Match 36.5%; Score 54; DB 1; Length 92;
Best Local Similarity 90.0%; Pred. No. 0.97; 1; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 18 SLHWSYGLRP 27
DB 23 SQHWSYGLRP 32

RESULT 6
RHPGG
gonadoliberin - pig
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 18-Mar-1997
C:Accession: A01411
R:Baba, Y.; Matsuo, H.; Schally, A.V.
Biochem. Biophys. Res. Commun. 44, 459-463, 1971
A:Title: Structure of the porcine LH- and FSH-releasing hormone. II. Confirmation of t
A:Reference number: A90172; MUID:72114303; PMID:4946067
A:Accession: A01411
A:Molecule type: protein
A:Residues: 1-10 <BAB>
R:Matsuo, H.; Arimura, A.; Nair, R.M.G.; Schally, A.V.
Biochem. Biophys. Res. Commun. 45, 822-827, 1971
A:Title: Synthesis of the porcine LH- and FSH-releasing hormone by the solid-phase met
A:Reference number: A90176; MUID:72065376; PMID:4942726
A:Contents: annotation; synthesis
A:Note: the synthetic and natural hormones have the same physicochemical and biologica
R:Baba, Y.; Arimura, A.; Schally, A.V.
Biochem. Biophys. Res. Commun. 45, 483-487, 1971
A:Title: On the tryptophan residue in porcine LH and FSH-releasing hormone.
A:Reference number: A90175; MUID:72117544; PMID:4946275
A:Contents: annotation
A:Note: Trp-3 appears to be essential for biological activity
C:Comment: This hypothalamic hormone stimulates the secretion of both luteinizing and
C:Superfamily: gonadoliberin
C:Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:10/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 35.1%; Score 52; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 HWSYGLRP 27
DB 2 HWSYGLRP 9

RESULT 7
RHSRG
gonadoliberin - sheep
C:Species: Ovis orientalis aries. Ovis ammon aries (domestic sheep)
C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 18-Mar-1997
C:Accession: A93780; A01411
R:Burgus, R.; Butcher, M.; Amoss, M.; Ling, N.; Monahan, M.; Rivier, J.; Fellows, R.;
Proc. Natl. Acad. Sci. U.S.A. 69, 278-282, 1972
A:Title: Primary structure of the ovine hypothalamic luteinizing hormone-releasing fac
A:Reference number: A93780; MUID:72094314; PMID:4550508
A:Accession: A93780
A:Molecule type: protein
A:Residues: 1-10 <BUR>
A:Note: the natural and synthetic hormones have the same biological activity
C:Comment: This hypothalamic hormone stimulates the secretion of both luteinizing and
C:Superfamily: gonadoliberin
C:Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:10/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 35.1%; Score 52; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.18;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 HWSYGLRP 27
 |||||
 Db 2 HWSYGLRP 9

RESULT 8
 151423
 gonadoliberin precursor - African clawed frog
 N:Alternate names: luteinizing hormone releasing hormone
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999
 C:Accession: I51423
 R:Hayes, W.P.; Wray, S.; Battey, J.F.
 Endocrinology 134, 1835-1845, 1994
 A:Title: The frog GnRH-I gene has a mammalian-like expression pattern and conserved domain
 A:Reference number: 151423; MUID:94185563; PMID:8137750
 A:Accession: I51423
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-89 <HAY>
 A:Cross-references: GB:I28040; NID:G496291; PIDN:AAA49728.1; PID:G496292
 C:Genetics:
 A:Gene: GnRH-I
 C:Superfamily: gonadoliberin

Query Match 35.1%; Score 52; DB 2; Length 89;
 Best Local Similarity 100.0%; Pred. No. 1-8;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 HWSYGLRP 27
 |||||
 Db 25 HWSYGLRP 32

RESULT 9
 AD3098
 periplasmic nitrate reductase large subunit [imported] - Agrobacterium tumefaciens (stra
 C:Species: Agrobacterium tumefaciens
 C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
 C:Accession: AD3098
 R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I
 erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell
 i; Karp, P.; Romero, P.; Zhang, S.
 Science 294, 2317-2323, 2001
 A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
 ster, E.W.
 A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A:Reference number: AB2577; MUID:21608550; PMID:11743193
 A:Accession: AD3098
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-824 <KUR>
 A:Cross-references: GB:AB208689; PIDN:AA445202.1; PID:G17742881; GSFDB:GN00187
 A:Experimental source: strain C58 (Dupont)
 C:Genetics:
 A:Gene: napA
 A:Map position: linear chromosome
 C:Superfamily: Alcaligenes eutrophus nitrate reductase A chain

Query Match 34.8%; Score 51.5; DB 2; Length 824;
 Best Local Similarity 37.0%; Pred. No. 24;
 Matches 10; Conservative 9; Mismatches 1; Indels 7; Gaps 2;

QY 2 YIKANSKFI-GITELGSLHWSYGLRP 27
 |||||
 Db 279 FVRNHTKFRVGVTDIG-----YGLRP 299

RESULT 10
 E98188
 periplasmic nitrate reductase precursor napA (AF040988) [imported] - Agrobacterium tumef

C:Species: Agrobacterium tumefaciens
 C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002
 C:Accession: E98188
 R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldmar
 A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.
 Science 294, 2323-2328, 2001
 A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tu
 A:Reference number: A97359; MUID:21608551; PMID:11743194
 A:Accession: E98188
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-834 <KUR>
 A:Cross-references: GB:AB007870; PIDN:AAK89031.1; PID:G15158825; GSFDB:GN00170
 C:Genetics:
 A:Gene: AGR L 917
 A:Map position: linear chromosome
 C:Superfamily: Alcaligenes eutrophus nitrate reductase A chain

Query Match 34.8%; Score 51.5; DB 2; Length 834;
 Best Local Similarity 37.0%; Pred. No. 24;
 Matches 10; Conservative 9; Mismatches 1; Indels 7; Gaps 2;

QY 2 YIKANSKFI-GITELGSLHWSYGLRP 27
 |||||
 Db 289 FVRNHTKFRVGVTDIG-----YGLRP 309

RESULT 11
 C72710
 probable fmu protein APE1098 - Aeropyrum pernix (strain K1)
 C:Species: Aeropyrum pernix
 C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
 C:Accession: C72710
 R:Kawarayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Taka
 awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.;
 DNA Res. 6, 83-101, 1999
 A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy
 A:Reference number: A72450; MUID:99310339; PMID:10382966
 A:Accession: C72710
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-388 <KAW>
 A:Cross-references: DBJ:AP000050; NID:G5104188; PIDN:BAA80083.1; PID:G1043869; PID:G51
 A:Experimental source: strain K1
 C:Genetics:
 A:Gene: APE1098

Query Match 34.5%; Score 51; DB 2; Length 388;
 Best Local Similarity 71.4%; Pred. No. 12;
 Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 14 ELGPSLHWSYGLRP 27
 |||||
 Db 345 ELGPFELTWSYGLRP 358

RESULT 12
 S29982
 class II histocompatibility antigen - Atlantic salmon
 C:Species: Salmo salar (Atlantic salmon)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Sep-1999
 C:Accession: S29982
 R:Hardvik, I.
 submitted to the EMBL Data Library, October 1992
 A:Reference number: S29980
 A:Accession: S29982
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-244 <HOR>
 A:Cross-references: EMBL:X70166; NID:G64369; PID:G64370
 C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 34.1%; Score 50.5; DB 2; Length 244;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 10, 2004, 08:58:53 ; Search time 5.12062 Seconds
(without alignments)
284.724 Million cell updates/sec

Title: US-09-848-834A-11

Perfect score: 148

Sequence: 1 QYIKANSKFIGITELGSLHWSYGLRPX 28

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	74	50.0	1314	1 TETX_CLOTE	P04958 Clostridium
2	54	36.5	67	1 GONI_MACMU	P55247 macaca mula
3	54	36.5	90	1 GONI_MOUSE	P13562 mus musculus
4	54	36.5	91	1 GONI_PIG	P49921 sus scrofa
5	54	36.5	92	1 GONI_HUMAN	P01148 homo sapien
6	54	36.5	92	1 GONI_RAT	P07490 rattus norv
7	52	35.1	61	1 GONI_SHEEP	Q28588 ovnis aries
8	52	35.1	63	1 GONI_MESAU	O09163 mesocricetu
9	52	35.1	89	1 GONI_XENLA	P45656 xenopus lae
10	52	35.1	90	1 GONI_RANCA	Q90y63 rana catesb
11	52	35.1	92	1 GONI_TUPGB	Q95335 tupaia glis
12	49	33.1	452	1 YD04_SCHPO	O14197 schizosacch
13	49	33.1	3133	1 HMCT_BOMMO	P98092 bombyx mori
14	48	32.4	10	1 GONI_ALLMI	P37041 alligator m
15	48	32.4	92	1 GONI_CAVPO	O54713 cavia porce
16	48	32.4	92	1 GONI_CHICK	P37042 gallus gall
17	47	31.8	216	1 YD04_LEPIN	P59247 leptospira
18	46	31.1	94	1 GONI_HAPBU	P73812 haplochromi
19	46	31.1	95	1 GONI_MORSA	O51918 morone saxa
20	46	31.1	95	1 GONI_PAGMA	P70074 pagrus majo
21	46	31.1	95	1 GONI_SPAAU	P51919 sparus auro
22	46	31.1	99	1 GONI_DICLA	P70074 dicentrarch
23	46	31.1	110	1 YHBU_ACTAC	P96769 actinobacil
24	46	31.1	459	1 DCUC_VIBCH	Q9K156 vibrio chol
25	46	31.1	780	1 PPSA_DEIRA	O83026 deinococcus
26	45.5	30.7	322	1 YAU8_SCHPO	Q10166 schizosacch
27	45	30.4	258	1 MIP_CHLPN	Q9Z7P3 chlamydia p
28	45	30.4	347	1 A11C_MOUSE	Q9GZW0 mus musculu
29	45	30.4	644	1 YHJ9_YEAST	P38694 saccharomyc
30	45	30.4	674	1 AGUA_THEMEA	P36105 thermotoga
31	45	30.4	831	1 NAPA_ALCEU	P39185 alcaligenes
32	44	29.7	66	1 VG84_BPMLS	Q05301 mycobacteri
33	44	29.7	90	1 GON8_RANDY	Q91au2 rana dybows

ALIGNMENTS

RESULT 1

TETX_CLOTE
ID TETX_CLOTE STANDARD; PRT; 1314 AA.

AC P04958; 1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 13-AUG-1987 (Rel. 05, Last annotation update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tetanus toxin precursor [EC 3.4.24.68] (Tentoxylisin) [Contains:
Tetanus toxin light chain (Tetanus toxin chain L); Tetanus toxin heavy
chain (Tetanus toxin chain H)].
DE chain (Tetanus toxin chain H)].
GN TETX OR CTP80.
OS Clostridium tetani.
OC Plasmiid pE88, and Plasmid 75 Kbp.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1513;
RN [1]
RP SEQUENCE FROM N.A.
RC PLASMID=75 Kbp;
RX MEDLINE=87053814; PubMed=3536478;
RA Eisel U., Jarausch W., Goretzki K., Henschen A., Engels J.,
Waller U., Hudel M., Habermann E., Niemann H.;
RT "Tetanus toxin: primary structure, expression in E. coli, and
homology with botulinum toxins.";
RT EMBO J. 5:2495-2502(1986).
RL Nucleic Acids Res. 14:7809-7812(1986).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CN3911; PLASMID=75 Kbp;
RX STRAIN=CN3911; PubMed=3774547;
RA Fairweather N.F., Lyness V.A.;
RT "The complete nucleotide sequence of tetanus toxin.";
RT Nucleic Acids Res. 14:7809-7812(1986).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Massachusetts / E88; PLASMID=pE88;
RX MEDLINE=22457253; PubMed=12552129;
RA Brueggemann H., Baumer S., Fricke W.F., Wierse A., Liesegang H.,
Decker I., Herzberg C., Martinez-Arias R., Merkl R., Henne A.,
Gottschalk G.;
RT "The genome sequence of Clostridium tetani, the causative agent of
tetanus disease.";
RT Proc. Natl. Acad. Sci. U.S.A. 100:1316-1321(2003).
RN [4]
RP SEQUENCE OF 742-1314 FROM N.A.
RC PLASMID=75 Kbp;
RX MEDLINE=86085672; PubMed=3510187;
RA Fairweather N.F., Lyness V.A., Fickard D.J., Allen G., Thomson R.O.;
RT "Cloning, nucleotide sequencing, and expression of tetanus toxin
fragment C in Escherichia coli.";
RN J. Bacteriol. 165:21-27(1986).
RN [5]
RP PARTIAL SEQUENCE, AND DISULFIDE BONDS.
RX MEDLINE=30201034; PubMed=2108021;
RA Kriegstein K., Henschen A., Waller U., Habermann E.;
RT "Arrangement of disulfide bridges and positions of sulfhydryl groups
in tetanus toxin.";

P37545 bacillus su
Q58778 methanococ
O78450 guillardia
Q09305 caenorhabdi
P53083 saccharomyc
P19721 mouse adeno
P56161 anopheles s
P32176 escherichia
Q91409 dicentrarch
Q9kct3 bacillus ha
O06737 bacillus su
Q82267 chlamydomphi

RL Eur. J. Biochem. 188:39-45(1990).
 RN [6]
 RP PARTIAL SEQUENCE.
 RX MEDLINE=92037649; PubMed=1935979;
 RA Krieglstein K.G., Henschen A.H., Weller U., Habermann E.;
 RT "limited proteolysis of tetanus toxin. Relation to activity and
 identification of cleavage sites.";
 RL Eur. J. Biochem. 202:41-51(1991).
 RN [7]
 RP IDENTIFICATION OF SUBSTRATE.
 RX MEDLINE=93010948; PubMed=1396558;
 RA Schiavo G., Poulain B., Rossetto O., Benfenati F., Tauc L.,
 RA Montecucco C.;
 RT "Tetanus toxin is a zinc protein and its inhibition of
 neurotransmitter release and protease activity depend on zinc.";
 RL EMBO J. 11:3577-3583(1992).
 RN [8]
 RP IDENTIFICATION OF SUBSTRATE.
 RX MEDLINE=93063293; PubMed=1331807;
 RA Schiavo G., Benfenati F., Poulain B., Rossetto O., de Laureto P.P.,
 RA Dasgupta B.R., Montecucco C.;
 RT "Tetanus and botulinum-B neurotoxins block neurotransmitter release
 by proteolytic cleavage of synaptobrevin.";
 RL Nature 359:832-835(1992).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 874-1314.
 RX MEDLINE=97475217; PubMed=9334741;
 RA Umland T.C., Wingert L.M., Swaminathan S., Furey W.P., Schmidt J.J.,
 RA Sax M.;
 RT "Structure of the receptor binding fragment HC of tetanus
 neurotoxin.";
 RL Nat. Struct. Biol. 4:788-792(1997).
 CC -!- FUNCTION: TETANUS TOXIN ACTS BY INHIBITING NEUROTRANSMITTER
 RELEASE. IT BINDS TO PERIPHERAL NEURONAL SYNAPSES, IS INTERNALIZED
 AND MOVES BY RETROGRADE TRANSPORT UP THE AXON INTO THE SPINAL CORD
 WHERE IT CAN MOVE BETWEEN POSTSYNAPTIC AND PRESYNAPTIC NEURONS. IT
 INHIBITS NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC
 ENDOPEPTIDASE THAT CATALYZES THE HYDROLYSIS OF THE 76-GLN-|-PHE-77
 BOND OF SYNAPTOSOMAL-2.
 CC -!- CATALYTIC ACTIVITY: Hydrolysis of 76-Gln-|-Phe-77 bond in
 synaptobrevin 2.
 CC -!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
 CC -!- SUBUNIT: THE PRECURSOR POLYPEPTIDE IS SUBSEQUENTLY CLEAVED TO
 YIELD SUBCHAINS L AND H. THESE REMAIN LINKED BY A DISULFIDE BRIDGE
 AND ARE NON-TOXIC AFTER SEPARATION.
 CC -!- MISCELLANEOUS: THE C-TERMINAL OF THE HEAVY CHAIN BINDS TO
 GLYCOSIDE RECEPTORS.
 CC -!- SIMILARITY: Belongs to peptidase family M27.
 CC -----
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 or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL; X04436; CAA28033.1; --
 DR EMBL; X06214; CAA29564.1; --
 DR EMBL; AF528097; AAO37454.1; --
 DR EMBL; M12739; AAZ3282.1; --
 DR FIR; A25689; BTCLTN.
 DR PDB; IAF9; 29-APR-98.
 DR PDB; IAS8; 14-OCT-98.
 DR PDB; IDOH; 27-MAR-00.
 DR PDB; IDFQ; 24-MAR-00.
 DR PDB; IDIW; 24-MAR-00.
 DR PDB; IDLL; 24-MAR-00.
 DR PDB; IFV3; 05-SEP-01.
 DR MEROPS; M27.001; --
 DR InterPro; IPR008985; Cona_like lec_gl.
 DR InterPro; IPR002160; Kunitz legume.
 DR InterPro; IPR006025; Pept_M_Zn_BS.
 DR InterPro; IPR000395; Peptidase_M27.
 DR Pfam; PF01742; Peptidase_M27; 1.
 DR PRINTS; PR00760; BONTOKILYSIN.
 DR PRODOM; PD001963; Bontokilysin; 1.
 DR PROSITE; PS00142; ZINC PROTEASE; 1.
 KW Neurotoxin; Transmembrane; Hydrolase; Metalloprotease; Zinc; Plasmid;
 KW 3D-structure; Complete proteome.
 FT INIT_MET 0
 FT CHAIN 1 456 TETANUS TOXIN LIGHT CHAIN.
 FT CHAIN 457 1314 TETANUS TOXIN HEAVY CHAIN.
 FT METAL 232 ZINC (CATALYTIC) (BY SIMILARITY).
 FT ACT_SITE 233 BY SIMILARITY.
 FT METAL 236 ZINC (CATALYTIC) (BY SIMILARITY).
 FT TRANSMEM 226 246 POTENTIAL.
 FT TRANSMEM 669 689 POTENTIAL.
 FT DISULFID 438 466 INTERCHAIN.
 FT DISULFID 1076 1092
 FT HELIX 876 882
 FT TURN 883 883
 FT STRAND 884 891
 FT TURN 892 893
 FT STRAND 894 897
 FT STRAND 904 907
 FT TURN 909 910
 FT STRAND 912 915
 FT STRAND 920 925
 FT TURN 928 929
 FT STRAND 932 935
 FT HELIX 938 940
 FT TURN 941 946
 FT STRAND 949 956
 FT HELIX 962 968
 FT TURN 969 970
 FT STRAND 972 977
 FT STRAND 980 981
 FT HELIX 983 985
 FT STRAND 987 995
 FT TURN 996 997
 FT STRAND 998 1004
 FT TURN 1006 1007
 FT STRAND 1010 1016
 FT TURN 1020 1020
 FT TURN 1021 1022
 FT STRAND 1031 1037
 FT TURN 1039 1040
 FT STRAND 1042 1047
 FT TURN 1048 1049
 FT STRAND 1050 1056
 FT TURN 1058 1059
 FT STRAND 1068 1074
 FT TURN 1079 1080
 FT STRAND 1082 1091
 FT HELIX 1097 1105
 FT TURN 1106 1107
 FT STRAND 1112 1112
 FT STRAND 1114 1114
 FT TURN 1116 1117
 FT STRAND 1120 1120
 FT STRAND 1122 1122
 FT TURN 1123 1124
 FT STRAND 1127 1131
 FT HELIX 1132 1134
 FT TURN 1135 1136
 FT STRAND 1137 1141
 FT TURN 1144 1145
 FT STRAND 1148 1152
 FT STRAND 1155 1158
 FT TURN 1159 1162
 FT STRAND 1163 1166
 FT STRAND 1173 1178
 FT TURN 1184 1188
 FT STRAND 1188 1190
 FT STRAND 1190 1190

Query Match 50.0%; Score 74; DB 1; Length 1314;
 Best Local Similarity 100.0%; Pred. No. 0.0044;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QYKANSKFIGITEL 15
 |||||
 DB 829 QYKANSKFIGITEL 843

RESULT 2
 GONI_MACMU STANDARD; PRT; 67 AA.
 AC P55247;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Progonadoliberein I precursor [Contains: Gonadoliberein I (LH-RH I)]
 DE (Luteinizing hormone-releasing hormone I) (Gonadotropin-releasing hormone I) (GnRH I) (Luliberin I); GnRH-associated peptide I] (Fragment).
 DE (GnRH I) OR GnRH OR LHRH.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Hypothalamus;
 RX MEDLINE=95124501; PubMed=7545971;
 RA Ma Y.J., Costa M.E., Ojeda S.R.;
 RT "Developmental expression of the genes encoding transforming growth factor alpha and its receptor in the hypothalamus of female rhesus macaques";
 RL Neuroendocrinology 60:346-359(1994).
 CC -!- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates the secretion of both luteinizing and follicle-stimulating hormones.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the GnRH family.
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 CC -----
 DR EMBL; S75918; AAB33096.1; -
 DR PIR; I78541; I78541.
 DR InterPro; IPR002012; GnRH.
 DR Pfam; PF00446; GnRH; 1.
 DR PRINTS; PR01541; GonadolibereinI.
 DR PROSITE; PS00473; GnRH; 1.
 KW Cleavage on pair of basic residues; Hormone; Amidation; Hypothalamus; Signal; Pyroglutamate carboxylic acid.
 FT SIGNAL 1 1
 FT NON_TER 1 1
 FT SIGNAL <1 5 BY SIMILARITY.
 FT CHAIN 6 >67 PROGNADOLIBERIN I.
 FT PEPTIDE 6 15 GONADOLIBERIN I.
 FT PEPTIDE 19 >67 GnRH-ASSOCIATED PEPTIDE I.
 FT ACT_SITE 8 8 APPEARS TO BE ESSENTIAL FOR BIOLOGICAL ACTIVITY (BY SIMILARITY).
 FT MOD_RES 6 6 PYRROLIDONE CARBOXYLIC ACID (BY SIMILARITY).
 FT MOD_RES 15 15 AMIDATION (G-16 PROVIDE AMIDE GROUP) (BY SIMILARITY).
 FT NON_TER 67 67
 FT SEQUENCE 67 AA; 7573 MW; 505394DAA261A3F2 CRC64;

Query Match 36.5%; Score 54; DB 1; Length 67;
 Best Local Similarity 90.0%; Pred. No. 0.23;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 18 SLHWSYGLRP 27
 |||||
 DB 5 SQHWSYGLRP 14

RESULT 3
 GONI_MOUSE STANDARD; PRT; 90 AA.
 AC F13562;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Progonadoliberein I precursor [Contains: Gonadoliberein I (LH-RH I)]
 DE (Luteinizing hormone-releasing hormone I) (Gonadotropin-releasing hormone I) (GnRH I) (Luliberin I); Prolactin release-inhibiting factor I].
 DE GnRH1 OR GnRH.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87069928; PubMed=3024317;
 RA Mason A.J., Haylick J.S., Zoeller R.T., Young W.S. III, Phillips H.S., Nikolics K., Seeburg P.H.;
 RT "A deletion truncating the gonadotropin-releasing hormone gene is responsible for hypogonadism in the hpg mouse";
 RL Science 234:1366-1371(1986).
 CC -!- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates the secretion of both luteinizing and follicle-stimulating hormones.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the GnRH family.
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 CC -----
 DR EMBL; M14872; AAA37717.1; -
 DR PIR; A4578; RMSG.
 DR MGD; MGI:95789; GnRH.
 DR InterPro; IPR002012; GnRH.
 DR InterPro; IPR004079; GonadolibereinI.
 DR Pfam; PF00446; GnRH; 1.
 DR PRINTS; PR01541; GonadolibereinI.
 DR PROSITE; PS00473; GnRH; 1.
 KW Cleavage on pair of basic residues; Hormone; Amidation; Hypothalamus; Placenta; Signal; Pyroglutamate carboxylic acid.
 FT SIGNAL 1 21
 FT CHAIN 22 90 PROGNADOLIBERIN I.
 FT PEPTIDE 22 31 GONADOLIBERIN I.
 FT PEPTIDE 35 90 PROLACTIN RELEASE-INHIBITING FACTOR I.
 FT ACT_SITE 24 24 APPEARS TO BE ESSENTIAL FOR BIOLOGICAL ACTIVITY.
 FT MOD_RES 22 22 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 31 31 AMIDATION (G-32 PROVIDE AMIDE GROUP).
 FT SEQUENCE 90 AA; 10337 MW; 1C0766FA4826E4D9 CRC64;
 QY 18 SLHWSYGLRP 27
 |||||

Query Match 36.5%; Score 54; DB 1; Length 90;
 Best Local Similarity 90.0%; Pred. No. 0.31;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 21 SQHWSYGLRP 30

RESULT 4

GN1_PIG STANDARD; PRT; 91 AA.

AC P4921; 1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Progonadolibarin I precursor [Contains: Gonadolibarin I (LH-RH I)]

DE (Luteinizing hormone-releasing hormone I) (Gonadotropin-releasing hormone I) (GnRH I) (Luliberin I); GnRH-associated peptide I.

GN GNRI OR GNRIH

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OX NCBI_TaxID=9823;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE-Hypothalamus;

RA Wesner G.D., Matteri R.L., Becker B.A.;

RL Submitted (MAY-1994) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE OF 24-33.

RX MEDLINE=72114303; PubMed=4946067;

RA Baba Y., Matsuo H., Schally A.V.;

RT "Structure of the porcine LH- and FSH-releasing hormone. II. Confirmation of the proposed structure by conventional sequential analyses".

RL Biochem. Biophys. Res. Commun. 44:459-463 (1971).

RN [3]

RP SYNTHESIS OF GONADOLIBERIN.

RX MEDLINE=72065376; PubMed=4942726;

RA Matsuo H., Arimura A., Nair R.M.G., Schally A.V.;

RT "Synthesis of the porcine LH- and FSH-releasing hormone by the solid-phase method".

RL Biochem. Biophys. Res. Commun. 45:822-827 (1971).

RN [4]

RP SYNTHESIS OF GONADOLIBERIN.

RX MEDLINE=72117544; PubMed=4946275;

RA Baba Y., Arimura A., Schally A.V.;

RT "On the tryptophan residue in porcine LH and FSH-releasing hormone.";

RL Biochem. Biophys. Res. Commun. 45:483-487 (1971).

CC 1- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates the secretion of both luteinizing and follicle-stimulating hormones.

CC 1- SUBCELLULAR LOCATION: Secreted.

CC 1- SIMILARITY: Belongs to the GnRH family.

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CC EMBL: L32864; AAA31066.1; -

DR InterPro; IPR002012; GnRH.

DR InterPro; IPR004079; GonadolibarinI.

DR Pfam; PF00446; GnRH; 1.

DR PRINTS; PR01541; GONADOLIBERIN.

DR PROSITE; PS00473; GNRIH; 1.

KW Cleavage on pair of basic residues; Hormone; Amidation; Hypothalamus; Placenta; Signal; Pyrrolidone carboxylic acid.

FT SIGNAL 1 23

FT CHAIN 24 91

FT PEPTIDE 24 33

FT GONADOLIBERIN I.

FT ACT_SITE 26 26

FT ACT_SITE 26 26

FT MOD_RES 24 24

FT PYRROLIDONE CARBOXYLIC ACID.

FT MOD_RES 33 33

SQ SEQUENCE 91 AA; 10090 MW; 8340474F32DDAA99 CRC64;

AMIDATION (G-34 PROVIDE AMIDE GROUP).

Query Match 36.5%; Score 54; DB 1; Length 91;

Best Local Similarity 90.0%; Pred. No. 0.32;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 18 SLHWSYGLRP 27

DB 23 SQHWSYGLRP 32

RESULT 5

GN1_HUMAN STANDARD; PRT; 92 AA.

AC P01148.

DT 21-JUL-1986 (Rel. 01, Created)

DT 01-APR-1988 (Rel. 07, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Progonadolibarin I precursor [Contains: Gonadolibarin I (LH-RH I)]

DE (Luteinizing hormone-releasing hormone I) (Gonadotropin-releasing hormone I) (GnRH I) (Luliberin I) (Gonadorelin); GnRH-associated peptide I.

GN GNRI OR GNRIH OR LHRH.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=89366682; PubMed=2671939;

RA Hayflick J.S., Adelman J.P., Seeburg P.H.;

RT "The complete nucleotide sequence of the human gonadotropin-releasing hormone gene".

RL Nucleic Acids Res. 17:6403-6403 (1989).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=86094338; PubMed=2867548;

RA Adelman J.P., Mason A.J., Hayflick J.S., Seeburg P.H.;

RT "Isolation of the gene and hypothalamic cDNA for the common precursor of gonadotropin-releasing hormone and prolactin release-inhibiting factor in human and rat".

RL Proc. Natl. Acad. Sci. U.S.A. 83:179-183 (1986).

RN [3]

RP SEQUENCE FROM N.A. AND VARIANT SER-16.

RX MEDLINE=86012739; PubMed=6090951;

RA Seeburg P.H., Adelman J.P.;

RT "Characterization of cDNA for precursor of human luteinizing hormone releasing hormone".

RL Nature 311:666-668 (1984).

RN [4]

RP SEQUENCE OF 24-33.

RX MEDLINE=8126573; PubMed=6760865;

RA Tan L., Rousseau P.;

RT "The chemical identity of the immunoreactive LHRH-like peptide biosynthesized in the human placenta".

RL Biochem. Biophys. Res. Commun. 109:1061-1071 (1982).

RN [5]

RP VARIANT SER-16.

RX MEDLINE=99318093; PubMed=10391209;

RA Cargill M., Altshuler D., Ireland J., Sklar P., Ardlie K., Patil N., Shaw N., Lane C.R., Lim E.P., Kalyanaram N., Nemesh J., Ziaugra L., Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q., Lander E.S.;

RT "Characterization of single-nucleotide polymorphisms in coding regions of human genes".

RL Nat. Genet. 22:231-238 (1999).

RN [6]

RP ERRATUM.

RA Cargill M., Altshuler D., Ireland J., Sklar P., Ardlie K., Patil N., Shaw N., Lane C.R., Lim E.P., Kalyanaram N., Nemesh J., Ziaugra L., Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q., Lander E.S.;

RL Nat. Genet. 23:373-373(1999).
 CC -!- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates
 CC the secretion of both luteinizing and follicle-stimulating
 CC hormones.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- PHARMACOLOGICAL: Available under the names Factivel (Ayerst Labs),
 CC Lutrepulse or Lutrelf (Ferring Pharmaceuticals) and Relisorm
 CC (Serono).
 CC -!- SIMILARITY: Belongs to the GnRH family.
 CC -----
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 CC -----
 CC EMBL; X01059; CAA5526.1; -;
 CC EMBL; M12578; AAA35916.1; -;
 CC EMBL; X15215; CAA33285.1; -;
 CC PIR; S05308; RHUG.
 CC Genew; HGNC:4419; GNRH1.
 CC MIM; 152760; -;
 CC GO; GO:0005625; C:soluble fraction; TAS.
 CC GO; GO:0005183; F:luteinizing hormone-releasing factor activity; TAS.
 CC GO; GO:0007267; P:cell-cell signaling; TAS.
 CC GO; GO:0007275; P:development; TAS.
 CC GO; GO:0008285; P:negative regulation of cell proliferation; TAS.
 CC GO; GO:0007165; P:signal transduction; TAS.
 CC InterPro; IPR002012; GNRH
 CC InterPro; IPR004079; Gonadoliberin1.
 CC Pfam; PF00446; GNRH; 1.
 CC PRINTS; PR01541; GONADOLIBERN1.
 CC PROSITE; PS00473; GNRH; 1.
 CC Cleavage on pair of basic residues; Hormone; Amidation; Hypothalamus;
 CC Placenta; Pharmaceutical; Signal; Polymorphism;
 CC Pyroglutamate carboxylic acid.
 CC SIGNAL 1 23
 CC CHAIN 24 92 PROGNADOLIBERIN I.
 CC PEPTIDE 24 33 GONADOLIBERIN I.
 CC PEPTIDE 37 92 GNRH-ASSOCIATED PEPTIDE I.
 CC ACT_SITE 26 26 APPEARS TO BE ESSENTIAL FOR BIOLOGICAL
 CC ACTIVITY.
 CC MOD_RES 24 24 PYRROLIDONE CARBOXYLIC ACID.
 CC MOD_RES 33 33 AMIDATION (G-34 PROVIDE AMIDE GROUP).
 CC VARIANT 16 16 W -> S (in dbSNP:6185).
 CC FT FTID=VAR 013943.
 CC SQ SEQUENCE 92 AA; 10380 MW; 30A72221B076FA79 CRC64;
 Query Match 36.5%; Score 54; DB 1; Length 92;
 Best Local Similarity 90.0%; Pred. No. 0.32;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 18 SLHWSYGLRP 27
 Db 23 SQHWSYGLRP 32
 RESULT 6
 ID GON1_RAT STANDARD; PRT; 92 AA.
 AC P07490;
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Prognadoliberin I precursor [Contains: Gonadoliberin I (LH-RH I)
 DE (luteinizing hormone-releasing hormone I) (Gonadotropin-releasing
 DE hormone I) (GnRH I) (Luliberin I); Prolactin release-inhibiting factor
 DE I].
 DE GNRH1 OR GNRH.
 GN Rattus norvegicus (Rat).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CC NCBI_TaxID=10116;
 CC [1]
 CC SEQUENCE FROM N.A.
 CC MEDLINE=86094338; PubMed=2867548;
 CC Adelman J.P., Mason A.J., Hayflick J.S., Seeburg P.H.;
 CC "Isolation of the gene and hypothalamic cDNA for the common precursor
 CC of gonadotropin-releasing hormone and prolactin release-inhibiting
 CC factor in human and rat.";
 CC Proc. Natl. Acad. Sci. U.S.A. 83:179-183(1986).
 CC [2]
 CC SEQUENCE FROM N.A.
 CC MEDLINE=99384661; PubMed=2476669;
 CC Bond C.T., Hayflick J.S., Seeburg P.H., Adelman J.P.;
 CC "The rat gonadotropin-releasing hormone: SH locus: structure and
 CC hypothalamic expression";
 CC Mol. Endocrinol. 3:1257-1262 (1989).
 CC [3]
 CC SEQUENCE FROM N.A.
 CC TISSUE=Thymus;
 CC MEDLINE=93105480; PubMed=1468115;
 CC Maier C.C., Marchetti B., Leboeuf R.D., Blalock J.E.;
 CC "Thymocytes express a mRNA that is identical to hypothalamic
 CC luteinizing hormone-releasing hormone mRNA.";
 CC Cell. Mol. Neurobiol. 12:447-454(1992).
 CC [4]
 CC SEQUENCE OF 1-47 FROM N.A.
 CC TISSUE=Heart;
 CC MEDLINE=87149087; PubMed=3547652;
 CC Adelman J.P., Bond C.T., Douglass J., Herbert E.;
 CC "Two mammalian genes transcribed from opposite strands of the same
 CC DNA locus.";
 CC Science 235:1514-1517(1987).
 CC -!- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates
 CC the secretion of both luteinizing and follicle-stimulating
 CC hormones.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Central nervous system.
 CC -!- SIMILARITY: Belongs to the GnRH family.
 CC -----
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 CC -----
 CC EMBL; S08070; AAB24572.1; -;
 CC EMBL; M12579; AAA41263.1; -;
 CC EMBL; M31670; AAA41264.1; -;
 CC EMBL; M15527; AAA42141.1; ALT_SEQ.
 CC EMBL; M15529; AAA42139.1; -;
 CC EMBL; M15528; -; NOT_ANNOTATED_CDS.
 CC PIR; A40147; RHRTG.
 CC InterPro; IPR002012; GNRH.
 CC InterPro; IPR004079; Gonadoliberin1.
 CC Pfam; PF00446; GNRH; 1.
 CC PRINTS; PR01541; GONADOLIBERN1.
 CC PROSITE; PS00473; GNRH; 1.
 CC Cleavage on pair of basic residues; Hormone; Amidation; Hypothalamus;
 CC Placenta; Signal; Pyroglutamate carboxylic acid.
 CC SIGNAL 1 23
 CC CHAIN 24 92 PROGNADOLIBERIN I.
 CC PEPTIDE 24 33 GONADOLIBERIN I.
 CC PEPTIDE 37 92 PROLACTIN RELEASE-INHIBITING FACTOR I.
 CC ACT_SITE 26 26 APPEARS TO BE ESSENTIAL FOR BIOLOGICAL
 CC ACTIVITY.
 CC MOD_RES 24 24 PYRROLIDONE CARBOXYLIC ACID.
 CC MOD_RES 33 33 AMIDATION (G-34 PROVIDE AMIDE GROUP).
 CC SEQUENCE 92 AA; 10500 MW; 494B5C64DA8A3EB3 CRC64;
 Query Match 36.5%; Score 54; DB 1; Length 92;

Best Local Similarity 90.0%; Pred. No. 0.32;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 18 SLHWSYGLRP 27
| | | | |
Dp 23 SOHWSYGLRP 32

RESULT 7	CONI_SHEEP	STANDARD;	PRT;	61 AA.
ID	GONT_SHEEP			
AC	Q28588;			
DT	15-DEC-1998 (Rel. 37, Created)			
DT	15-DEC-1998 (Rel. 37, Last annotation update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Progonadoliberin I precursor (Contains: Gonadoliberin I (LH-RH I) (Luteinizing hormone-releasing hormone I) (Gonadotropin-releasing hormone I) (GnRH I) (Luliberin I); GnRH-associated peptide I) (Fragment)			
DE	(Fragment)			
DE	GNRH1 OR GNRH OR LHRH.			
OS	Ovis aries (Sheep).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Euteria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
OC	Bovidae; Caprinae; Ovis.			
OX	NCBI_TaxID=9940;			
OX	[1]			
RN	SEQUENCE OF 12-61 FROM N.A.			
RP	STRAIN=Western range; TISSUE=Hypothalamus;			
RC	Rodríguez R.E., Wise M.B.;			
RL	Submitted (Oct-1993) to the ENBL/GenBank/DBJ databases.			

Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 8; Conservative 0; Mismatches 0; Indels 0;
Caps 0;

QY 20 HWSYGLRP 27
| | | | |
Db 2 HWSYGLRP 9

```

RESULT 8
GONI_MESAU STANDARD; PRT; 63 AA.
ID GONI_MESAU
AC 009163;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Progonaadoliberin I precursor [Contains: Gonadoliberin I (LH-RH I)
DE (Luteinizing hormone-releasing hormone I) (Gonadotropin-releasing
DE hormone I) (GnRH I) (Luliberin I); GnRH-associated peptide I]
DE (Fragment).
DE GNRH1 OR GNRH OR LHRH.
GN Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OC NCBI_TaxID=10036;
RN [1]
RN SEQUENCE FROM N.A.
RA Jansen H.T., Stevens P.J., Zeitler P., Lehman M.N.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates
CC the secretion of both luteinizing and follicle-stimulating
CC hormones.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the GnRH family.

```

Qy 20 HWSYGLRP 27
db 2 HWSYGLRP 9

DE (Luteinizing hormone releasing hormone I) (Gonadotropin releasing hormone I) (GnRH I) (Luliberin I); GnRH-associated peptide I (GAP1)).
GN GNRH1 OR GNRH.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.
OX NCBI_TaxID=8400;
RN [1]
RN SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND DEVELOPMENTAL STAGE.
RP TISSUE=Forebrain;
RX MEDLINE=21102951; PubMed=11170016;
RA Wang L., Yoo M.S., Kang H.M., Im W.B., Choi H.S., Bogerd J.,
RA Kwon H.B.;
RT "Cloning and characterization of cDNAs encoding the GNRH1 and GNRH2
RT precursors from bullfrog (Rana catesbeiana).";
RL J. Exp. Zool. 289:190-201 (2001).
CC -!- FUNCTION: Stimulates the secretion of gonadotropins (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Forebrain.
CC -!- DEVELOPMENTAL STAGE: Expressed at significantly higher levels
CC during post-breeding. Not expressed in pituitary.
CC -!- SIMILARITY: Belongs to the GnRH family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF188754; AAL05972.1;
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0005183; F:luteinizing hormone-releasing factor activity; NAS.
DR GO; GO:0009755; P:hormone mediated signaling; NAS.
DR GO; GO:0000003; P:reproduction; NAS.
DR InterPro; IPR002012; GnRH.
DR InterPro; IPR004079; Gonadoliberin1.
DR Pfam; PF00446; GnRH; 1.
DR PRINTS; PR01541; GONADOLIBERN1.
DR PROSITE; PS00473; GnRH; 1.
KW Cleavage on pair of basic residues; Hormone; Amidation; Signal;
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 90 PROGONADOLIBERIN I.
FT PEPTIDE 25 34 GONADOLIBERIN I.
FT PEPTIDE 38 86 GnRH-ASSOCIATED PEPTIDE I (BY
FT MOD_RES 25 25 SIMILARITY).
FT MOD_RES 34 34 PYRROLIDONE CARBOXYLIC ACID (BY
FT MOD_RES 34 34 SIMILARITY).
FT MOD_RES 34 34 AMIDATION (G-35 PROVIDE AMIDE GROUP) (BY
FT MOD_RES 34 34 SIMILARITY).
SQ SEQUENCE 90 AA; 10291 MW; 317203B4E3DA2FE7 CRC64;
Query Match 35.1%; Score 52; DB 1; Length 90;
Best Local Similarity 100.0%; Pred. No. 0.63; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Mismatches 0; Mismatches 0;
QY 20 HWSYGLRP 27
DB 26 HWSYGLRP 33
RESULT 11
GN1_TUPGB STANDARD; PRT; 92 AA.
ID GN1_TUPGB
AC Q95335;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Progonadoliberin I precursor [Contains: Gonadoliberin I (LHRH I)
DE (Luteinizing hormone-releasing hormone I) (Gonadotropin-releasing

RESULT 9
GN1_XENLA STANDARD; PRT; 89 AA.
AC P45566;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Gonadoliberin I precursor (Gonadotropin-releasing hormone I) (GnRH-I)
DE (LH-RH) (Luliberin I).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RN SEQUENCE FROM N.A.
RP TISSUE=Forebrain;
RX MEDLINE=94185563; PubMed=8137750;
RA Hayes W.P., Wray S., Battey J.F.;
RT "The frog gonadotropin-releasing hormone-I (GnRH-I) gene has a
RT mammalian-like expression pattern and conserved domains in
RT GnRH-associated peptide, but brain onset is delayed until
RT metamorphosis.";
RL Endocrinology 134:1835-1844 (1994).
CC -!- FUNCTION: Stimulates the secretion of gonadotropins.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the GnRH family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; L28040; AAA49728.1;
DR PIR; I51423; I51423.
DR InterPro; IPR002012; GnRH.
DR InterPro; IPR004079; Gonadoliberin1.
DR Pfam; PF00446; GnRH; 1.
DR PRINTS; PR01541; GONADOLIBERN1.
DR PROSITE; PS00473; GnRH; 1.
KW Cleavage on pair of basic residues; Hormone; Amidation; Hypothalamus;
FT SIGNAL 1 23
FT CHAIN 24 89 PROGONADOLIBERIN I.
FT PEPTIDE 24 33 GONADOLIBERIN I.
FT PEPTIDE 37 89 GONADOTROPIN-RELEASING HORMONE ASSOCIATED
FT PEPTIDE.
FT PEPTIDE 37 85 GnRH-ASSOCIATED PEPTIDE I (GAP).
FT MOD_RES 24 24 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 33 33 AMIDATION (G-34 PROVIDE AMIDE GROUP).
SQ SEQUENCE 89 AA; 10246 MW; 6F4F36FBAE0D4284 CRC64;
Query Match 35.1%; Score 52; DB 1; Length 89;
Best Local Similarity 100.0%; Pred. No. 0.63; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Mismatches 0; Mismatches 0;
QY 20 HWSYGLRP 27
DB 25 HWSYGLRP 32
RESULT 10
GN1_RANCA STANDARD; PRT; 90 AA.
ID GN1_RANCA
AC Q90V63;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Progonadoliberin I precursor [Contains: Gonadoliberin I (LHRH I)
DE (Luteinizing hormone-releasing hormone I) (Gonadotropin-releasing

DE hormone I) (Gnrh I) (Luliberin I); Gnrh-associated peptide II.
GN GNRH1 OR GNRH.
OS Tupaiia glis belangeri (Common tree shrew).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Scandentia; Tupaiidae; Tupaiia.
OX NCBI_TaxID=37347;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Hypothalamus.
RX MEDLINE=97079639; PubMed=8921350;
RA Kasten T.L., White S.A., Norton T.T., Bond C.T., Adelman J.P.,
RA Fernald R.D.;
RT "Characterization of two new preproGnrh mRNAs in the tree shrew:
RT first direct evidence for mesencephalic Gnrh gene expression in a
RT placental mammal";
RL Gen. Comp. Endocrinol. 104:7-19 (1996).
CC -!- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates
CC the secretion of both luteinizing and follicle-stimulating
CC hormones.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the Gnrh family.
CC
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CC
CC EMBL; U63326; AAB16837.1; -.
DR InterPro; IPR002012; Gnrh.
DR InterPro; IPR004079; Gonadoliberin1.
DR Pfam; PF00446; Gnrh; 1.
DR PRINTS; PR01541; GONADOLIBERN1.
DR PROSITE; PS00473; GNRH; 1.
KW Cleavage on pair of basic residues; Hormone; Amidation; Hypothalamus;
KW Placenta; Signal; Pyrrolidone carboxylic acid.
FT SIGNAL 1 23
FT CHAIN 24 92
FT PEPTIDE 24 33
FT PEPTIDE 37 92
FT ACT_SITE 26 26
FT MOD_RES 24 24
FT MOD_RES 33 33
FT MOD_RES 33 33
SQ SEQUENCE 92 AA; 10197 MW; 4FDBF2C58CF5F63B CRC64;
Query Match 35.1%; Score 52; DB 1; Length 92;
Best Local Similarity 100.0%; Pred. No. 0.65;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 20 HWSYGLRP 27
DB 25 HWSYGLRP 32
RESULT 12
ID YDQ4 SCHPO STANDARD; PRT; 452 AA.
AC O14197;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein C5D6.04 in chromosome I.
GN SPAC5D6.04.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;

[1]
RN SEQUENCE FROM N.A.
RP STRAIN=972; PubMed=11859360;
RX MEDLINE=21848401; Rayndream M.A., Lyne M., Lyne R., Stewart A.,
RA Wood V., Gwilliam R., Rajandream M.A., Baker S., Basham D., Bowman S.,
RA Sgourou J., Peat N., Hayles J., Chillingworth T., Churcher C.M.,
RA Brooks K., Brown D., Brown S., Collins M., Collins P., Feltwell T., Fraser A.,
RA Collins M., Connor R., Cronin A., Davis P., Hidalgo J., Hodgson G.,
RA Gattles S., Goble A., Hamlin N., Harris D., Huckle E.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volkert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Gloux S., Lelaure V., Mottier S.,
RA Goffeau A., Cadieu E., Dreano S., Hunt C., Moore K., Hurst S.M.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado I., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsberg S.L.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe";
RL Nature 415:871-880 (2002).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC
CC -!- SIMILARITY: TO YEAST YER287W
CC
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CC
CC EMBL; Z98056; CAB10852.1; -.
DR FIR; T38962; T38962.
DR GenesDB_Spombe; SPAC5D6.04; -.
DR InterPro; IPR004776; Auxin eff.
DR Pfam; PF03547; Auxin eff; 1.
KW Hypothetical protein; Transmembrane.
FT TRANSMEM 18 38
FT TRANSMEM 81 101
FT TRANSMEM 269 289
FT TRANSMEM 317 337
FT TRANSMEM 354 374
FT TRANSMEM 390 410
FT TRANSMEM 428 448
SQ SEQUENCE 452 AA; 49575 MW; 71B77EA5725C69A8 CRC64;
Query Match 33.1%; Score 49; DB 1; Length 452;
Best Local Similarity 57.1%; Pred. No. 9.2;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 13 TELGPSLHWSYGLR 26
DB 166 SQLQALRWSYGYR 179
RESULT 13
HMCT BOMMO
ID HMCT BOMMO STANDARD; PRT; 3133 AA.
AC P98032;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Hemocytin precursor (Humoral lectin).

OS Bombyx mori (Silk moth).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea;
 OC Bombycidae; Bombyx.
 OX NCBI_TaxID=7091;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FUYOU X Tokai; TISSUE=Hemocyte;
 RX MEDLINE=55178544; PubMed=7873598;
 RA Kotani E., Yamakawa M., Iwamoto S.-I., Tashiro M., Mori H., Sumida M.,
 RA Matsubara F., Tanai K., Kadoh-Okuda K., Kato Y., Mori H.;
 RA "Cloning and expression of the gene of hemocytin, an insect humoral
 RT lectin which is homologous with the mammalian von Willebrand
 RT factor";
 RL Biochim. Biophys. Acta 1260:245-258(1995).
 RN [2]
 RP SEQUENCE OF 2221-3133 FROM N.A.
 RA Kotani E., Iwamoto S.-I., Tashiro M., Mori H., Sumida M.,
 RA Matsubara F., Yamakawa M.;
 RL Submitted (JAN-1993) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Adhesive protein and relates to hemostasis or
 CC encapsulation of foreign substances for self-defense.
 CC -1- DEVELOPMENTAL STAGE: Expressed in hemocytes during larval-pupal
 CC metamorphosis.
 CC -1- INDUCTION: Hemagglutination activity is increased by bacterial
 CC or viral infection and inhibited by D-mannose, N-acetyl-D-
 CC galactosamine and D-maltose.
 CC -1- PTM: May be converted into the 260 kDa mature hemocytin by
 CC proteolysis.
 CC -1- SIMILARITY: TO MAMMALIAN VON WILLEBRAND FACTOR.
 CC -1- SIMILARITY: THIS N-TERMINAL DOMAIN SHOWS SOME SIMILARITY TO THAT
 CC OF HUMAN MUCIN 2.
 CC -1- SIMILARITY: Contains 2 F5/8 type C domains.
 CC -1- SIMILARITY: Contains 1 C-terminal cysteine knot-like (CTCK) domain.
 CC -----
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 CC -----
 DR ENBL; D29738; BAA06160.1; -;
 DR ENBL; D14035; BAA03124.1; -;
 DR PIR; S52093; S52093.
 DR HSSP; P12259; 1CZT.
 DR InterPro; IPR006207; Cys knot C.
 DR InterPro; IPR000421; FAS8 C.
 DR InterPro; IPR008973; Gal Bind like.
 DR InterPro; IPR002172; LDL_receptor_A.
 DR InterPro; IPR002919; TIL_Cysrich.
 DR InterPro; IPR001007; VWFC_C.
 DR Pfam; PF00754; F5_F8_type_C; 2.
 DR Pfam; PF01826; TIL; 2.
 DR Pfam; PF00094; vwd; 3.
 DR SMART; SM00041; CT; 1.
 DR SMART; SM00231; FAS8C; 2.
 DR SMART; SM00192; LDL; 1.
 DR SMART; SM00216; VWD; 3.
 DR PROSITE; PS01185; CTCK_1; 1.
 DR PROSITE; PS01225; CTCK_2; 1.
 DR PROSITE; PS01285; FAS8C_1; 2.
 DR PROSITE; PS01285; FAS8C_2; 2.
 DR PROSITE; PS00022; FAS8C_3; 2.
 DR PROSITE; PS01208; VWFC_1; FALSE NEG.
 DR LECTIN; Glycoprotein; Signal; Repeat; Cell adhesion.
 KW LECTIN; ?
 FT SIGNAL ? 3133 POTENTIAL.
 FT CHAIN 29 131
 FT DOMAIN 153 240
 FT DOMAIN D';
 FT DOMAIN D';

FT DOMAIN 248 613
 FT DOMAIN 940 1095
 FT DOMAIN 1116 1254
 FT DOMAIN 1283 1356
 FT DOMAIN 1620 1951
 FT DOMAIN 1952 2315
 FT DOMAIN 2320 2321
 FT DOMAIN 2335 2361
 FT DOMAIN 2435 2469
 FT DOMAIN 2553 2622
 FT DOMAIN 2842 2907
 FT DOMAIN 2971 3076
 FT DOMAIN 895 914
 FT DOMAIN 1267 1270
 FT DOMAIN 1425 1428
 FT DOMAIN 1447 1450
 FT DOMAIN 1474 1479
 FT DOMAIN 2148 2153
 FT DOMAIN 2156 2159
 FT DOMAIN 2341 2344
 FT DOMAIN 940 1095
 FT DISULFID 1116 1254
 FT DISULFID 2981 3040
 FT DISULFID 2991 3054
 FT DISULFID 3004 3070
 FT DISULFID 3020 3072
 FT DISULFID ? 3075
 FT CARBOHYD 151 151
 FT CARBOHYD 237 237
 FT CARBOHYD 564 564
 FT CARBOHYD 1170 1170
 FT CARBOHYD 1387 1387
 FT CARBOHYD 1622 1622
 FT CARBOHYD 1727 1727
 FT CARBOHYD 1847 1847
 FT CARBOHYD 1975 1975
 FT CARBOHYD 1985 1985
 FT CARBOHYD 2093 2093
 FT CARBOHYD 2113 2113
 FT CARBOHYD 2161 2161
 FT CARBOHYD 2276 2276
 FT CARBOHYD 2451 2451
 FT CARBOHYD 2647 2647
 FT CARBOHYD 2654 2654
 FT CARBOHYD 2653 2653
 FT CARBOHYD 2794 2794
 FT CARBOHYD 2810 2810
 FT CARBOHYD 2865 2865
 FT CARBOHYD 2929 2929
 FT CARBOHYD 2964 2964
 FT CARBOHYD 3028 3028
 FT VARIANT 1288 1288
 FT VARIANT 1305 1305
 SQ SEQUENCE 3133 AA; 343350 MW; E5210D5D14A7B2B2 CRC64;
 Query Match 33.1%; Score 49; DB 1; Length 3133;
 Best Local Similarity 50.0%; Pred. No. 65;
 Matches 9; Conservative 2; Mismatches 7; Indels 0; Gaps 0;
 QY 9 FGIETELGPSLHWSYGLR 26
 DB 346 FLDVPSLGLMSLQWDRGLR 363
 RESULT 14
 GONI_ALLMI
 ID GONI_ALLMI STANDARD; PRT; 10 AA.
 AC P37041; P20407;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Gonadoliberin I (Gonadotropin-releasing hormone I) (GNRH-I) (LH-RH I)
 DE (Luliberin I).

```

OS Alligator mississippiensis (American alligator).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Crocodylidae; Alligatorinae; Alligator.
OX NCBI_TaxID=8496;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=91352338; PubMed=1892082;
RA Lovejoy D.A., Fischer W.H., Parker D.B., McRory J.E., Park M.,
RA Lance V., Swanson P., Rivier J.E., Sherwood N.M.;
RT "Primary structure of two forms of gonadotropin-releasing hormone
RT from brains of the American alligator (Alligator mississippiensis).";
RL Regul. Pept. 33:105-115(1991).
CC -!- FUNCTION: Stimulates the secretion of gonadotropins.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the GnRH family.
DR PIR; A60066; RHAQ1.
DR InterPro; IPR002012; GnRH.
DR Pfam; PF00446; GnRH; 1.
DR PROSITE; PS00473; GnRH; 1.
KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.
FT MOD_RES 10 10 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1172 MW; 284B23D7286B45A3 CRC64;

Query Match 32.4%; Score 48; DB 1; Length 10;
Best Local Similarity 87.5%; Pred. No. 0.28;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Caps 0;

QY 20 HWSYGLRP 27
DB 2 HWSYGLQP 9

RESULT 15
GONL_CAVPO STANDARD; PRT; 92 AA.
ID GONL_CAVPO
AC 054713;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Progonadoliberein I precursor [Contains: Gonadoliberein I (LH-RH I)
DE (Luteinizing hormone-releasing hormone I) (Gonadotropin-releasing
DE hormone I) (GnRH I) (Luliberin I); GnRH-associated peptide I].
GN GnRH1 OR GnRH OR LHRH.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Hartley white; TISSUE=Hypothalamus;
RX MEDLINE=97462693; PubMed=9322920;
RA Jimenez-Linan M., Rubin B.S., King J.C.;
RT "Examination of guinea pig luteinizing hormone-releasing hormone gene
RT reveals a unique decapeptide and existence of two transcripts in the
RT brain";
RL Endocrinology 138:4123-4130(1997).
CC -!- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates
CC the secretion of both luteinizing and follicle-stimulating
CC hormones.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the GnRH family.
CC
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CC
CC EMBL; AF033346; AAB87688.1; -

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DR InterPro; IPR002012; GnRH.
DR InterPro; IPR004079; Gonadoliberein1.
DR PRINTS; PR01541; GONADOLIBERN1.
DR PROSITE; PS00473; GnRH; 1.
KW Cleavage on pair of basic residues; Hormone; Amidation; Hypothalamus;
KW Placenta; Signal; Pyrrolidone carboxylic acid.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 1 23 PROGONADOLIBERIN I.
FT PEPTIDE 24 92 GONADOLIBERIN I.
FT PEPTIDE 24 33 GnRH-ASSOCIATED PEPTIDE I.
FT ACT_SITE 26 26 APPEARS TO BE ESSENTIAL FOR BIOLOGICAL
FT ACT_SITE 26 26 ACTIVITY (BY SIMILARITY).
FT MOD_RES 24 24 PYRROLIDONE CARBOXYLIC ACID (BY
FT MOD_RES 24 24 SIMILARITY).
FT MOD_RES 33 33 AMIDATION (G-34 PROVIDE AMIDE GROUP) (BY
FT MOD_RES 33 33 SIMILARITY).
SQ SEQUENCE 92 AA; 10279 MW; ACF74613F456D663 CRC64;

Query Match 32.4%; Score 48; DB 1; Length 92;
Best Local Similarity 57.1%; Pred. No. 2.6;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Caps 0;

QY 14 ELGSLHWSYGLRP 27
DB 19 ENGSGQYWSYGVRP 32

Search completed: March 10, 2004, 09:13:54
Job time : 5.12062 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 10, 2004, 08:58:54 ; Search time 13.1634 Seconds
(without alignments)
133.345 Million cell updates/sec

Title: US-09-848-834A-10
Perfect score: 186
Sequence: 1 FNNFTVSWLVRPKVSASHLEGPLHWSYGLRPX 34

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep: *
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep: *
3: /cgn2_6/ptodata/2/iaa/5A_COMB.pep: *
4: /cgn2_6/ptodata/2/iaa/5B_COMB.pep: *
5: /cgn2_6/ptodata/2/iaa/5A_COMB.pep: *
6: /cgn2_6/ptodata/2/iaa/5B_COMB.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	152	81.7	32	1 US-08-446-692-14
2	152	81.7	32	2 US-08-488-381A-14
3	116	62.4	188	4 US-09-396-937-14
4	114	61.3	173	4 US-09-396-937-20
5	112	60.2	21	1 US-07-610-525-1
6	112	60.2	21	2 US-08-661-052-12
7	112	60.2	21	2 US-08-460-502-8
8	112	60.2	21	2 US-08-724-774B-5
9	112	60.2	21	3 US-09-089-595-5
10	112	60.2	21	3 US-09-382-855-5
11	112	60.2	21	3 US-09-183-714B-5
12	112	60.2	21	3 US-09-188-082-12
13	112	60.2	21	3 US-09-171-969-10
14	112	60.2	21	4 US-09-364-088-12
15	112	60.2	21	4 US-09-642-281-5
16	112	60.2	21	4 US-09-102-716-12
17	112	60.2	21	4 US-08-432-483A-3
18	112	60.2	21	4 US-08-148-711A-8
19	112	60.2	21	4 US-09-589-717-5
20	112	60.2	21	4 US-08-945-289-3
21	112	60.2	21	4 US-09-396-937-35
22	112	60.2	21	4 US-09-405-986A-2
23	112	60.2	21	5 PCT-US93-11703-66
24	112	60.2	31	5 PCT-US93-11703-64
25	112	60.2	452	1 US-07-618-312A-2
26	112	60.2	452	1 US-07-618-312A-4
27	112	60.2	452	1 US-08-110-786A-8

28	112	60.2	452	1	US-08-280-228-2	Sequence 2, Appli
29	112	60.2	452	1	US-08-280-228-4	Sequence 4, Appli
30	112	60.2	618	1	US-08-668-381A-5	Sequence 5, Appli
31	112	60.2	853	4	US-08-913-880C-17	Sequence 17, Appli
32	112	60.2	858	4	US-08-913-880C-16	Sequence 16, Appli
33	112	60.2	860	4	US-08-913-880C-15	Sequence 15, Appli
34	112	60.2	862	4	US-08-913-880C-14	Sequence 14, Appli
35	112	60.2	865	4	US-08-913-880C-13	Sequence 13, Appli
36	112	60.2	866	4	US-08-913-880C-12	Sequence 12, Appli
37	112	60.2	874	4	US-08-913-880C-11	Sequence 11, Appli
38	112	60.2	875	4	US-08-913-880C-10	Sequence 10, Appli
39	112	60.2	1315	4	US-08-913-880C-1	Sequence 1, Appli
40	107	57.5	22	1	US-08-446-692-5	Sequence 5, Appli
41	107	57.5	22	2	US-08-488-351A-5	Sequence 5, Appli
42	107	57.5	22	3	US-09-100-409A-41	Sequence 41, Appli
43	107	57.5	22	5	PCT-US95-13841-8	Sequence 8, Appli
44	100	53.8	19	1	US-07-610-525-2	Sequence 2, Appli
45	94.5	50.8	20	2	US-08-319-704-11	Sequence 11, Appli

ALIGNMENTS

RESULT 1
US-08-446-692-14
; Sequence 14, Application US/08446692
; Patent No. 5759551
; GENERAL INFORMATION:
; APPLICANT: Ladd, Anna
; APPLICANT: Wang, Chang Yi
; APPLICANT: Zamb, Timothy
; TITLE OF INVENTION: Immunogenic LHRH peptide constructs
; TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maria C.H. Lin
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,692
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria C.H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4146 US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)415-8745
; TELEFAX: (516)751-6849
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-446-692-14

Query Match 81.7%; Score 152; DB 1; Length 32;
Best Local Similarity 87.9%; Pred. No. 1.8e-15;
Matches 29; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

Qy 1 FNNFTVSWLVRPKVSASHLEGPLHWSYGLRP 33
Db 3 FNNFTVSWLVRPKVSASHLE---HWSYGLRP 31

RESULT 2
US-08-488-351A-14
; Sequence 14, Application US/08488351A
; Patent No. 5843446
; GENERAL INFORMATION:
; APPLICANT: Ladd, Anna
; APPLICANT: Wang, Chang Yi
; APPLICANT: Zaab, Timothy
; TITLE OF INVENTION: Immunogenic LHRH peptide constructs
; TITLE OF INVENTION: and synthetic universal immune stimulants for vaccines
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maria C.H. Lin
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10154-0053
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,351A
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/446,692
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/229,275
; FILING DATE: 14-APR-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/057,166
; FILING DATE: 27-APR-1992
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria C.H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4146 US2
; TELEPHONE: (212)415-8745
; TELEFAX: (516)751-8849
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-488-351A-14

Query Match 81.7%; Score 152; DB 2; Length 32;
Best Local Similarity 87.9%; Pred. No. 1.8e-15;
Matches 29; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

Qy 1 FNNFTVSFWLRVPKVSASHLEGPSLHWSYGLRP 33
Db 3 FNNFTVSFWLRVPKVSASHLE---HWSYGLRP 31

RESULT 3
US-09-396-937-14
; Sequence 14, Application US/09396937
; Patent No. 6645500
; GENERAL INFORMATION:
; APPLICANT: M&E Biotech A/S
; APPLICANT: HALKIER, Torben
; APPLICANT: HAANING, Jesper
; TITLE OF INVENTION: Method for Down-Regulating Osteoprotegerin Ligand

; TITLE OF INVENTION: Activity
; FILE REFERENCE: 22021 PC 1
; CURRENT APPLICATION NUMBER: US/09/396,937
; CURRENT FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion of
; OTHER INFORMATION: murine OPGL, residues 158-316 modified by
; OTHER INFORMATION: introduction of tetanus toxoid P30 epitope, and
; OTHER INFORMATION: His tag
US-09-396-937-14

Query Match 62.4%; Score 116; DB 4; Length 188;
Best Local Similarity 82.1%; Pred. No. 2.7e-09;
Matches 23; Conservative 1; Mismatches 0; Indels 4; Gaps 1;

Qy 1 FNNFTVSFWLRVPKVSASHLEGPSLHWS 28
Db 113 FNNFTVSFWLRVPKVSASHLE---NWS 136

RESULT 4
US-09-396-937-20
; Sequence 20, Application US/09396937
; Patent No. 6645500
; GENERAL INFORMATION:
; APPLICANT: M&E Biotech A/S
; APPLICANT: HALKIER, Torben
; APPLICANT: HAANING, Jesper
; TITLE OF INVENTION: Method for Down-Regulating Osteoprotegerin Ligand
; FILE REFERENCE: 22021 PC 1
; CURRENT APPLICATION NUMBER: US/09/396,937
; CURRENT FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 173
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion between
; OTHER INFORMATION: murine OPGL, residues 158-316 with tetanus toxoid
; OTHER INFORMATION: P30 epitope introduced, and His tag
US-09-396-937-20

Query Match 61.3%; Score 114; DB 4; Length 173;
Best Local Similarity 54.5%; Pred. No. 4.8e-09;
Matches 24; Conservative 2; Mismatches 2; Indels 16; Gaps 1;

Qy 1 FNNFTVSFWLRVPKVSASHLE-----GPSLHWS 28
Db 78 FNNFTVSFWLRVPKVSASHLEVTIKIPSSHNLMLKGGSTKNWS 121

RESULT 5
US-07-610-525-1
; Sequence 1, Application US/07610525
; Patent No. 5196512
; GENERAL INFORMATION:
; APPLICANT: BIANCHI Elisabetta
; APPLICANT: PESSI Antonello
; APPLICANT: CORRADIN Giampietro
; TITLE OF INVENTION: SYNTHETIC PEPTIDES USEFUL AS
; TITLE OF INVENTION: UNIVERSAL CARRIERS FOR THE PREPARATION OF IMMUNOGENIC CONJUGA
; TITLE OF INVENTION: AND THEIR USE IN THE DEVELOPMENT OF SYNTHETIC VACCINES.
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:

ADDRESSEE: SHEA & GOULD
STREET: 1251 AVENUE OF THE AMERICAS
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: UNITED STATES
ZIP: 10020-1193
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/610,525
FILING DATE: 19901108
CLASSIFICATION: 424
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-827-3000
TELEFAX: 212-840-6702
TELEX: 423973
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acid residues
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: no
FRAGMENT TYPE: internal fragment
US-07-610-525-1

Query Match 60.2%; Score 112; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.7e-10;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FNNFTVSWLRVPKVSASHLE 21
DB 1 FNNFTVSWLRVPKVSASHLE 21

RESULT 6
US-08-661-052-12
Sequence 12, Application US/08661052
Patent No. 5837243
GENERAL INFORMATION:
APPLICANT: Yashwant M. Deo
APPLICANT: Joel Goldstein
APPLICANT: Robert Graziano
APPLICANT: Chezian Somasundaram
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/661,052
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/484,172
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MXI-043CP

TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-661-052-12

Query Match 60.2%; Score 112; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.7e-10;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FNNFTVSWLRVPKVSASHLE 21
DB 1 FNNFTVSWLRVPKVSASHLE 21

RESULT 7
US-08-460-502-8
Sequence 8, Application US/08460502
Patent No. 5843464
GENERAL INFORMATION:
APPLICANT: Bakaletz, Lauren O.
APPLICANT: Kaumaya, Parvin T.
TITLE OF INVENTION: Synthetic Chimeric Fimbrin Peptides
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calfee, Halter and Griswold
STREET: 800 Superior Avenue
CITY: Cleveland
STATE: Ohio
COUNTRY: U.S.A.
ZIP: 44114-2688
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,502
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Golrick, Mary E.
REGISTRATION NUMBER: 34,829
REFERENCE/DOCKET NUMBER: 22727/00120
TELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 622-8458
TELEFAX: (216) 241-0816
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-460-502-8

Query Match 60.2%; Score 112; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.7e-10;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FNNFTVSWLRVPKVSASHLE 21
DB 1 FNNFTVSWLRVPKVSASHLE 21

RESULT 8
US-08-724-774B-5

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; Sequence 5, Application US/08724774B
; Patent No. 5908778
; GENERAL INFORMATION:
; APPLICANT: Rimoldi, Donata; Jongeneel, Victor; Coullie,
; APPLICANT: Pierre; Cerrottini, Jean-Charles; Carrel,
; APPLICANT: Stefan; Reed, Daryl
; TITLE OF INVENTION: WAGE-10 ENCODING cDNA, The Tumor
; TITLE OF INVENTION: Rejection Antigen Precursors Mage-10,
; TITLE OF INVENTION: Antibodies Specific to The Molecule, and
; TITLE OF INVENTION: Uses Thereof
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08724,774B
; FILING DATE: 03-October-1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Haneon, No. 5908778man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5457
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-724-774B-5
;
; Query Match 60.2%; Score 112; DB 2; Length 21;
; Best Local Similarity 100.0%; Pred. No. 7.7e-10;
; Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; Cy 1 FNNFTVSFWLRVPKVSASHLE 21
; Db 1 FNNFTVSFWLRVPKVSASHLE 21
;
; RESULT 9
; US-09-089-595-5
; Sequence 5, Application US/09089595
; Patent No. 6153728
; GENERAL INFORMATION:
; APPLICANT: Rimoldi, Donata; Jongeneel, Victor; Coullie,
; APPLICANT: Pierre; Cerrottini, Jean-Charles; Carrel,
; APPLICANT: Stefan; Reed, Daryl
; TITLE OF INVENTION: WAGE-10 ENCODING cDNA, The Tumor
; TITLE OF INVENTION: Rejection Antigen Precursors Mage-10,
; TITLE OF INVENTION: Antibodies Specific to The Molecule, and
; TITLE OF INVENTION: Uses Thereof
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
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; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/089,595
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,774
; FILING DATE: 03-October-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6153728man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5457
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21
; TYPE: amino acid
; TOPOLOGY: linear
; US-09-089-595-5
;
; Query Match 60.2%; Score 112; DB 3; Length 21;
; Best Local Similarity 100.0%; Pred. No. 7.7e-10;
; Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; Cy 1 FNNFTVSFWLRVPKVSASHLE 21
; Db 1 FNNFTVSFWLRVPKVSASHLE 21
;
; RESULT 10
; US-09-382-855-5
; Sequence 5, Application US/09382855
; Patent No. 6174692
; GENERAL INFORMATION:
; APPLICANT: Rimoldi, Donata; Jongeneel, Victor; Coullie, Pierre;
; APPLICANT: Cerrottini, Jean-Charles; Carrel, Stefan; Reed, Daryl
; TITLE OF INVENTION: WAGE-10 ENCODING cDNA, The Tumor Rejection
; TITLE OF INVENTION: Antigen Precursors Mage-10, Antibodies Specific To The Molecule
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski LLP
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/382,855
; FILING DATE: 25-August-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/089,595
; FILING DATE: 02-June-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,774
; FILING DATE: 03-October-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Schofield, Mary Anne
; REGISTRATION NUMBER: 36,669
; REFERENCE/DOCKET NUMBER: LUD 5457.2 DIV - JEL/NAS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
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;
; LENGTH: 21
; TYPE: amino acid
; TOPOLOGY: linear
US-09-382-855-5

Query Match
Best Local Similarity 60.2%; Score 112; DB 3; Length 21;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FNNFTVSFWLRVPKVSASHLE 21
Db 1 FNNFTVSFWLRVPKVSASHLE 21

RESULT 11
US-09-183-714B-5
; Sequence 5, Application US/09183714B
; Patent No. 6221593
; GENERAL INFORMATION:
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: Brasseur, Francis
; APPLICANT: Rimoldi, Donata
; APPLICANT: De Plaen, Etienne
; TITLE OF INVENTION: Method for Determining Cancer by Determining Expression
; TITLE OF INVENTION: OF MAGE-10
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/183,714B
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: US 08/724,774
; PRIOR FILING DATE: 1996-10-03
; NUMBER OF SEQ ID NOS: 7
; SEQ ID NO 5
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
US-09-183-714B-5

Query Match
Best Local Similarity 60.2%; Score 112; DB 3; Length 21;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FNNFTVSFWLRVPKVSASHLE 21
Db 1 FNNFTVSFWLRVPKVSASHLE 21

RESULT 12
US-09-188-082-12
; Sequence 12, Application US/09188082
; Patent No. 6270765
; GENERAL INFORMATION:
; APPLICANT: Yashwant M. Deo
; APPLICANT: Joel Goldstein
; APPLICANT: Robert Graziano
; APPLICANT: Chezhian Somasundaram
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
; TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/188,082
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; FILING DATE:
; PRIOR APPLICATION DATA: 08/661,052
; APPLICATION NUMBER: 08/661,052
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MXI-043CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; FRAGMENT TYPE: Internal
; US-09-188-082-12

Query Match
Best Local Similarity 60.2%; Score 112; DB 3; Length 21;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FNNFTVSFWLRVPKVSASHLE 21
Db 1 FNNFTVSFWLRVPKVSASHLE 21

RESULT 13
US-09-171-969-10
; Sequence 10, Application US/09171969
; Patent No. 6284533
; GENERAL INFORMATION:
; APPLICANT: Thomas, Lawrence J.
; TITLE OF INVENTION: PLASMID-BASED VACCINE FOR TREATING ATHEROSCLEROSIS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.
; STREET: 75 State Street, Suite 2300
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1807
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/171,969
; FILING DATE: 01 May 1997 (01.05.97)
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/640,713
; FILING DATE: 01 May 1996 (01.05.96)
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/802,967
; FILING DATE: 21 February 1997 (21.02.97)
; ATTORNEY/AGENT INFORMATION:
; NAME: Leon R. Yankwich
; REGISTRATION NUMBER: 30,237
; REFERENCE/DOCKET NUMBER: TCS 414.1 PCT (05872)
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL:
; ANTI-SENSE:
; FEATURE:
; NAME/KEY:
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LOCATION:
US-09-171-969-10

Query Match 60.2%; Score 112; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.7e-10;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FNNFTVSFWLRVPKVSASHLE 21
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DB 1 FNNFTVSFWLRVPKVSASHLE 21

RESULT 14

US-09-364-088-12
; Sequence 12, Application US/09364088
; Patent No. 6365161
; GENERAL INFORMATION:
; APPLICANT: Yashwant M. Deo, et al.
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
; OF ANTI-FC RECEPTOR ANTIBODIES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street, 24th Floor
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/364,088
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/188,082
; FILING DATE: 07-JUNE-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,172
; FILING DATE: 07-JUNE-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Remillard, Jane E.
; REGISTRATION NUMBER: 38,872
; REFERENCE/DOCKET NUMBER: MXI-043CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-7414
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-09-364-088-12

Query Match 60.2%; Score 112; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.7e-10;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FNNFTVSFWLRVPKVSASHLE 21
|||||
DB 1 FNNFTVSFWLRVPKVSASHLE 21

RESULT 15

US-09-642-281-5
; Sequence 5, Application US/09642281
; Patent No. 6387698
; GENERAL INFORMATION:
; APPLICANT: Rimoldi, Donata; Jongeneel, Victor; Coulie, Pierre;

;; Cerrottini, Jean-Charles; Carrel, Stefan; Reed, Daryl
;; TITLE OF INVENTION: MAGE-10 ENCODING CDNA, The Tumor Rejection
;; Antigen Precursors Mage-10, Antibodies Specific To The Molec
;;
;; NUMBER OF SEQUENCES: 5
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Fulbright & Jaworski LLP
;; STREET: 666 Fifth Avenue
;; CITY: New York City
;; STATE: New York
;; COUNTRY: USA
;; ZIP: 10103
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
;; COMPUTER: IBM
;; OPERATING SYSTEM: PC-DOS
;; SOFTWARE: Wordperfect
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/642,281
;; FILING DATE: 18-Aug-2000
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 09/089,595
;; FILING DATE: 02-June-1998
;; APPLICATION NUMBER: US 08/724,774
;; FILING DATE: 03-October-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Schofield, Mary Anne
;; REGISTRATION NUMBER: 36,669
;; REFERENCE/DOCKET NUMBER: LUD 5457.2 DIV - JEL/MAS
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 318-3000
;; TELEFAX: (212) 752-5958
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 21
;; TYPE: amino acid
;; TOPOLOGY: linear
;; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-642-281-5
Query Match 60.2%; Score 112; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 7.7e-10;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FNNFTVSFWLRVPKVSASHLE 21
|||||
DB 1 FNNFTVSFWLRVPKVSASHLE 21
Search completed: March 10, 2004, 09:28:54
Job time : 14.1634 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 10, 2004, 08:59:54 ; Search time 2.32296 seconds
(without alignments)
133.345 Million cell updates/sec

Title: US-09-848-834A-6

Perfect score: 29

Sequence: 1 SSGPSL 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA:*
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 - 2: /cgn2_6/prodata/2/iaa/5B_COMB.pep:*
 - 3: /cgn2_6/prodata/2/iaa/6A_COMB.pep:*
 - 4: /cgn2_6/prodata/2/iaa/6B_COMB.pep:*
 - 5: /cgn2_6/prodata/2/iaa/PCITUS_COMB.pep:*
 - 6: /cgn2_6/prodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	100.0	75	4	US-09-621-976-5469
2	29	100.0	147	4	US-09-252-991A-24435
3	29	100.0	200	3	US-09-181-183-38
4	29	100.0	200	4	US-09-280-040-38
5	29	100.0	200	4	US-09-277-700-38
6	29	100.0	200	4	US-09-874-585D-38
7	29	100.0	575	4	US-09-252-991A-17187
8	27	93.1	690	4	US-09-907-794A-49
9	27	93.1	690	4	US-09-905-125A-49
10	27	93.1	890	4	US-09-902-775A-49
11	27	93.1	888	4	US-08-956-242-4
12	27	93.1	888	3	US-09-351-215-4
13	26	89.7	20	3	US-08-658-857B-16
14	26	89.7	20	3	US-08-763-226C-16
15	26	89.7	20	3	US-09-307-200-16
16	26	89.7	20	4	US-09-593-321-16
17	26	89.7	20	4	US-09-030-619-117
18	26	89.7	21	6	5204096-18
19	26	89.7	76	4	US-09-205-258-892
20	26	89.7	119	4	US-09-252-991A-24599
21	26	89.7	179	4	US-09-461-325-345
22	26	89.7	179	4	US-10-012-542-345
23	26	89.7	215	4	US-09-252-991A-29779
24	26	89.7	320	4	US-09-716-129-77
25	26	89.7	332	4	US-09-198-452A-375
26	26	89.7	353	4	US-09-716-129-169
27	26	89.7	410	4	US-09-328-352-5085

28	26	89.7	477	4	US-09-252-991A-17030	Sequence 17030, A
29	26	89.7	480	4	US-09-543-681A-7592	Sequence 7592, Ap
30	26	89.7	802	4	US-09-173-151A-33	Sequence 33, Appl
31	26	89.7	855	4	US-08-890-865A-10	Sequence 10, Appl
32	26	89.7	971	3	US-09-107-149-19	Sequence 19, Appl
33	26	89.7	1036	3	US-08-968-752B-4	Sequence 4, Appl
34	26	89.7	1036	4	US-09-536-224-4	Sequence 4, Appl
35	26	89.7	1074	2	US-08-768-147B-2	Sequence 2, Appl
36	26	89.7	1074	3	US-08-968-752B-2	Sequence 2, Appl
37	26	89.7	1074	3	US-09-107-149-3	Sequence 3, Appl
38	26	89.7	1074	4	US-09-536-224-2	Sequence 2, Appl
39	26	89.7	1663	2	US-08-793-126-1	Sequence 1, Appl
40	26	89.7	1663	3	US-09-132-271-1	Sequence 1, Appl
41	26	89.7	1663	3	US-09-142-334-22	Sequence 22, Appl
42	26	89.7	3594	4	US-09-911-842A-4	Sequence 4, Appl
43	26	89.7	3969	3	US-08-061-376-5	Sequence 5, Appl
44	25	86.2	14	1	US-07-837-892-1	Sequence 1, Appl
45	25	86.2	15	1	US-07-837-892-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1

US-09-621-976-5469
; Sequence 5469, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621.976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 5469
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -70...-1
US-09-621-976-5469

Query Match 100.0%; Score 29; DB 4; Length 75;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 SSGPSL 6

Db 41 SSGPSL 46

RESULT 2

US-09-252-991A-24435
; Sequence 24435, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 24435
; LENGTH: 147

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; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24435

Query Match
Best Local Similarity 100.0%; Score 29; DB 4; Length 147;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSGPSL 6
Db 48 SSGPSL 53

RESULT 3
US-09-181-183-38
; Sequence 38, Application US/09181183
; Patent No. 6146866
; GENERAL INFORMATION:
; APPLICANT: VIITANEN, PAUL VEIKKO
; APPLICANT: BACOT, KAREN ONLEY
; TITLE OF INVENTION: LUMAZINE SYNTHASE AND
; RIBOFLAVIN SYNTHASE
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
; STREET: 1007 MARKET STREET
; CITY: WILMINGTON
; STATE: DELAWARE
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 19898
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.50 INCH
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: MICROSOFT WORD FOR WINDOWS 95
; SOFTWARE: MICROSOFT WORD VERSION 7.0A
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/280,040
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: FLOYD, LINDA AXAMETHY
; REGISTRATION NUMBER: 33,692
; REFERENCE/DOCKET NUMBER: CL-1083
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 302-992-8112
; TELEFAX: 302-773-0164
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 200 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: M. grisea LS
US-09-280-040-38

Query Match
Best Local Similarity 100.0%; Score 29; DB 4; Length 200;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSGPSL 6
Db 79 SSGPSL 84

RESULT 5
US-09-277-700-38
; Sequence 38, Application US/09277700
; Patent No. 6350597
; GENERAL INFORMATION:
; APPLICANT: VIITANEN, PAUL V.
; APPLICANT: BACOT, KAREN O.
; TITLE OF INVENTION: RIBOFLAVIN SYNTHASE GENES AND ENZYMES
; TITLE OF INVENTION: AND METHODS OF USE
; FILE REFERENCE: CL-1083-B
; CURRENT APPLICATION NUMBER: US/09/277,700
; CURRENT FILING DATE: 1999-03-26
; EARLIER APPLICATION NUMBER: 08/912,218
; EARLIER FILING DATE: AUGUST 15, 1997
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 38
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Magnaporthe grisea
US-09-277-700-38

Query Match
Best Local Similarity 100.0%; Score 29; DB 4; Length 200;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SSGPSL 6
Db 79 SSGPSL 84

RESULT 4
US-09-280-040-38
; Sequence 38, Application US/09280040
; Patent No. 6323013
; GENERAL INFORMATION:
; APPLICANT: VIITANEN, PAUL VEIKKO
```


Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSGPSL 6
|||||
Db 79 SSGPSL 84

RESULT 6

US-09-874-585D-38
; Sequence 38, Application US/09874585D
; Patent No. 6682891
; GENERAL INFORMATION:
; APPLICANT: E.I. DuPont de Nemours and Company, Inc.
; APPLICANT: VIITANEN, PAUL V.
; APPLICANT: BACOT, KAREN O.
; APPLICANT: JORDAN, DOUGLAS B.
; TITLE OF INVENTION: RIBOPOLYMER SYNTHASE GENES AND ENZYMES AND METHODS OF USE
; FILE REFERENCE: CL-1083-B
; CURRENT APPLICATION NUMBER: US/09/874,585D
; CURRENT FILING DATE: 1997-08-15
; PRIOR APPLICATION NUMBER: US 08/912,218
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Magnaporthe grisea
US-09-874-585D-38

Query Match 100.0%; Score 29; DB 4; Length 200;

Best Local Similarity 100.0%; Pred. No. 1.2e+02;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSGPSL 6
|||||
Db 79 SSGPSL 84

RESULT 7

US-09-252-991A-17187
; Sequence 17187, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17187
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17187

Query Match

Best Local Similarity 100.0%; Score 29; DB 4; Length 575;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSGPSL 6
|||||
Db 6 SSGPSL 11

RESULT 8

US-09-907-794A-49
; Sequence 49, Application US/09907794A

; Patent No. 6635458
; GENERAL INFORMATION:
; APPLICANT: Gerentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,794A
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1993-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 49
; LENGTH: 690
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-907-794A-49

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Query Match          93.1%; Score 27; DB 4; Length 690;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches      5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 SSGPSL 6
DB      414 SSGPSI 419

RESULT 9
US-09-905-125A-49
; Sequence 49, Application US/09905125A
; Patent No. 6664376
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc.
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Acids Encoding the Same
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,125A
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911

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; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
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; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 49
; LENGTH: 690
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-902-775A-49

Query Match 93.1%; Score 27; DB 4; Length 690;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SSGPSL 6
Db 414 SSGPSI 419

RESULT 11
US-08-956-242-4
; Sequence 4, Application US/08956242C
; Patent No. 5956081
; GENERAL INFORMATION:
; APPLICANT: Ganetzky, Barry S.
; APPLICANT: Titus, Steven A.
; TITLE OF INVENTION: Polynucleotides Encoding Herg-3
; FILE REFERENCE: 960296.94550
; CURRENT APPLICATION NUMBER: US/08/956,242C
; CURRENT FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 888
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; ORGANISM: Homo sapien
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; Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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; QY 1 SSGPSL 6
; DB 248 SSGPSI 253
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; RESULT 12
; US-09-351-215-4
; Sequence 4, Application US/09351215
; Patent No. 6087488
; GENERAL INFORMATION:
; APPLICANT: Ganetzky, Barry S.
; APPLICANT: Titus, Steven A.
; TITLE OF INVENTION: Polynucleotides Encoding Herg-3
; FILE REFERENCE: 960296.94550
; CURRENT APPLICATION NUMBER: US/09/351,215
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: 08/956,242
; EARLIER FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
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